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OM protein - protein search, using sw model

Run on: April 18, 2002, 09:26:52 ; Search time 23.84 Seconds  
(without alignments)  
105.641 Million cell updates/sec

Title: US-08-841-657A-2

Perfect score: 176

Sequence: 1 RRRGRSPRRTPSPRRRSKSPRRRSQSRSSQC.34

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 522463 seqs, 74073290 residues

Total number of hits satisfying chosen parameters: 522463

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_1101.\*

1:	/SID88/gcgdata/geneseq/geneseq/AA1980.DAT.*
2:	/SID88/gcgdata/geneseq/geneseq/AA1981.DAT.*
3:	/SID88/gcgdata/geneseq/geneseq/AA1982.DAT.*
4:	/SID88/gcgdata/geneseq/geneseq/AA1983.DAT.*
5:	/SID88/gcgdata/geneseq/geneseq/AA1984.DAT.*
6:	/SID88/gcgdata/geneseq/geneseq/AA1985.DAT.*
7:	/SID88/gcgdata/geneseq/geneseq/AA1986.DAT.*
8:	/SID88/gcgdata/geneseq/geneseq/AA1987.DAT.*
9:	/SID88/gcgdata/geneseq/geneseq/AA1988.DAT.*
10:	/SID88/gcgdata/geneseq/geneseq/AA1989.DAT.*
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12:	/SID88/gcgdata/geneseq/geneseq/AA1991.DAT.*
13:	/SID88/gcgdata/geneseq/geneseq/AA1992.DAT.*
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21:	/SID88/gcgdata/geneseq/geneseq/AA2000.DAT.*
22:	/SID88/gcgdata/geneseq/geneseq/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	176	100.0	34	AAW33686	Hbc nucleic acid-b
2	176	100.0	161	AAW33689	Recombinant protei
3	176	100.0	183	AAW33689	Hepatitis B virus
4	176	100.0	183	AAW33689	Hepatitis B virus
5	176	100.0	183	AAW33689	Hepatitis B virus
6	176	100.0	183	AAW33689	Hepatitis B virus
7	176	100.0	183	AAW33689	Hepatitis B virus
8	176	100.0	183	AAW33689	Hepatitis B virus
9	176	100.0	183	AAW33689	Hepatitis B virus
10	176	100.0	183	AAW33689	Hepatitis B virus
11	176	100.0	191	AAW33690	Recombinant protei

12	176	100.0	281	18	AAW33691	Nucleic acid-bound
13	176	100.0	456	18	AAW33693	Nucleic acid-bound
14	172	97.7	183	1	AAW33693	Sequence of core a
15	172	97.7	183	5	AAW33693	Hepatitis B virus co
16	172	97.7	183	11	AAW33693	Hepatitis B virus
17	172	97.7	183	14	AAW33693	Hepatitis B virus
18	172	97.7	183	14	AAW33693	Hepatitis B virus
19	172	97.7	183	15	AAW33693	Hepatitis B virus
20	172	97.7	183	16	AAW33693	Hepatitis B virus
21	172	97.7	183	16	AAW33693	Hepatitis B virus
22	172	97.7	183	16	AAW33693	Hepatitis B virus
23	172	97.7	183	16	AAW33693	Hepatitis B virus
24	172	97.7	183	16	AAW33693	Hepatitis B virus
25	172	97.7	183	19	AAW33693	Hepatitis B virus
26	172	97.7	183	20	AAW33693	Human hepatitis B
27	172	97.7	183	20	AAW33693	Human hepatitis B
28	172	97.7	183	21	AAW33693	Hepatitis B virus
29	172	97.7	183	22	AAW33693	Synthetic hepatitis
30	172	97.7	183	22	AAW33693	Viral protein sequ
31	172	97.7	183	1	AAW33693	Sequence of core a
32	172	97.7	183	9	AAW33693	Hepatitis B virus
33	172	97.7	193	19	AAW33693	Hepatitis B virus
34	172	97.7	196	14	AAW33693	Hepatitis B virus
35	172	97.7	198	14	AAW33693	Hepatitis B core /
36	172	97.7	198	14	AAW33693	Hepatitis B core /
37	172	97.7	208	14	AAW33693	Hepatitis B virus
38	172	97.7	212	19	AAW33693	Hepatitis B virus
39	172	97.7	212	21	AAW33693	Hepatitis B virus
40	172	97.7	212	21	AAW33693	Human hepatitis B
41	172	97.7	212	22	AAW33693	Hepatitis B virus
42	172	97.7	212	22	AAW33693	HBV genotype B pre
43	172	97.7	212	22	AAW33693	HBV genotype C pre
44	172	97.7	346	13	AAW33693	HBV genotype D pre
45	167	94.9	215	21	AAW33693	S12/core protein.
	166	94.3	183	16	AAW33693	HBV fusion protein
						Hepatitis B virus

## ALIGNMENTS

RESULT 1

AAW33686

ID AAW33686 standard; peptide; 34 AA.

AC AAW33686;

XX AAW33686;

XX AAW33686;

DT 30-APR-1998 (first entry)

XX Hbc nucleic acid-binding motif sequence.

DE Hbc nucleic acid-binding motif; Hbc; HBV; Hepatitis B virus; diagnosis;

KW HCV core polypeptide; immunosay; detection; antigen; disease;

KW Hepatitis C virus; infection.

XX Hepatitis B virus.

OS OS

XX EP805160-A1.

XX EP805160-A1.

PD 05-NOV-1997.

XX 05-NOV-1997.

PF 30-APR-1997; 97EP-0400985.

XX 01-MAY-1996; 96JP-0134444.

PR (FJRE ) FUJIREBIO INC.

XX Itoh S, Takemura F, Ueno E;

XX WPI: 1997-529030/49.

XX N-PSDB; AAV06334.

XX Nucleic acid-bound polypeptide - useful as immunoassay reagent

PS Claim 5; Page 16; 38pp; English.

XX This is a nucleic acid-binding motif present in the HBC protein of  
 CC Hepatitis B virus (HBV). This is fused to one terminus of a Hepatitis C  
 CC virus (HCV) core polypeptide. This is used in a method for producing a  
 CC nucleic acid-bound polypeptide. The method comprises producing a  
 CC fusion gene containing the polypeptide and the nucleic acid-binding  
 CC motif, binding a nucleic acid to the polypeptide as a soluble fraction,  
 CC and purifying the nucleic acid-bound polypeptide from the soluble  
 CC fraction. When the polypeptide is a recombinant form of an antigen, the  
 CC nucleic acid-bound polypeptide can be used as an immunoassay reagent for  
 CC detecting the antigen or an antibody to the antigen, especially in an  
 CC agglutination assay using particles coated with the nucleic acid-bound  
 CC polypeptide. The methods can be applied to diagnosis of disease and  
 CC infection, especially for the detection of HBV and HCV polypeptides.  
 CC The nucleic acid-bound polypeptides may be immunoreactive in cases where  
 CC the free polypeptide is not.  
 XX Sequence 34 AA;

Query Match 100.0%; Score 176; DB 18; Length 34;  
 Best Local Similarity 100.0%; Pred. No. 4,8e-14;  
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRGSPRRRTSPRRRSKSPRRRSQSRESQC 34  
 DB 1 rrrgsprrrtsprrrrsksprrrrsqresqc 34

RESULT 2  
 AAW33689  
 ID AAW33689 standard; Protein; 161 AA.  
 AC AAW33689;  
 DT 30-APR-1998 (first entry)  
 DE Recombinant protein 120NA.  
 KW Nucleic acid-binding motif; HCV; HBV; Hepatitis C virus; diagnosis;  
 KW core polypeptide; immunoassay; detection; antigen; disease; infection;  
 KW Hepatitis B virus; recombinant.  
 OS Synthetic.  
 OS Chimeric - Hepatitis C virus.  
 OS Chimeric - Hepatitis B virus.  
 XX EP805160-A1.  
 XX 05-NOV-1997.  
 XX 30-APR-1997; 97EP-0400985.  
 XX 01-MAY-1996; 96JP-0134444.  
 XX (FJRE ) FUJIREBIO INC.  
 XX Itoh S, Takemura F, Ueno E;  
 WPI; 1997-529030/49.  
 N-PSDB; AAV06337.  
 PT Nucleic acid-bound polypeptide - useful as immunoassay reagent

Example 1; Pages 20-21; 38pp; English.  
 This is a recombinant protein 120NA. This recombinant protein contains  
 the Hepatitis C virus (HCV) core polypeptide 120 fused to a nucleic  
 acid-binding motif present in the HBC protein of Hepatitis B virus  
 (HBV). This recombinant protein can be bound to a nucleic acid in the  
 host for producing a nucleic acid-bound polypeptide by a new method.  
 The method comprises producing a fusion gene containing the polypeptide  
 and the nucleic acid-binding motif, binding a nucleic acid to the

CC polypeptide as a soluble fraction, and purifying the nucleic acid-bound  
 CC polypeptide from the soluble fraction. When the polypeptide is a  
 CC recombinant form of an antigen, the nucleic acid-bound polypeptide can be  
 CC used as an immunoassay reagent for detecting the antigen or an antibody  
 CC to the antigen, especially in an agglutination assay using particles  
 CC coated with the nucleic acid-bound polypeptide. The methods can be  
 CC applied to diagnosis of disease and infection, especially for the  
 CC detection of HBV and HCV polypeptides. The nucleic acid-bound  
 CC polypeptides may be immunoreactive in cases where the free polypeptide  
 CC is not.  
 XX Sequence 161 AA;

Query Match 100.0%; Score 176; DB 18; Length 161;  
 Best Local Similarity 100.0%; Pred. No. 1.9e-13;  
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRGSPRRRTSPRRRSKSPRRRSQSRESQC 34  
 DB 128 rrrgsprrrtsprrrrsksprrrrsqresqc 161

RESULT 3  
 AAR98878  
 ID AAR98878 standard; protein; 183 AA.  
 AC AAR98878;  
 DT 29-AUG-1996 (first entry)  
 DE Hepatitis B virus E antigen (wild-type).  
 KW HBV; hepatitis B virus; antigen; HBeAg; specificity; diagnosis;  
 KW cross-reactivity.  
 XX Hepatitis B virus.  
 XX Location/Qualifiers  
 FH Key  
 FT Misc-difference 74...75 "mutation of Ser74 and/or Asn75 results in  
 FT a polypeptide having reduced cross-  
 FT reactivity with antibodies raised against  
 FT HBV c antigen"  
 XX JP08027185-A.  
 XX 30-JAN-1996.  
 XX 11-JUL-1994; 94JP-0180445.  
 XX 11-JUL-1994; 94JP-0180445.  
 XX (FJRE ) FUJI REBIO KK.  
 XX WPI; 1996-136327/14.  
 XX Novel anti-hepatitis-B-virus-e-antigen mutant for immuno:diagnosis  
 XX of hepatitis B - reacts specifically with anti-HBV-e-Ag antibody  
 XX without reacting with anti-HBV-c-Ag antibody

Disclosure; Page 5-6; 7pp; Japanese.  
 The present sequence is that of the wild-type e-antigen of  
 hepatitis B virus. This polypeptide is recognised both by  
 anti-HBeAg antibodies and by anti-HBcAg antibodies. To increase the  
 sensitivity of immunodiagnosis of hepatitis B, at least one of  
 residues 74 or 75 of the wild-type e-antigen is mutated. The  
 mutations result in antigens having reduced reactivity with anti-  
 HBcAg antibodies but which are still recognised by anti-HBeAg  
 antibodies. See AAR98879-R98885 for preferred mutants.  
 XX Sequence 183 AA;

```

Query Match      100.0%; Score 176; DB 17; Length 183;
Best Local Similarity 100.0%; Pred. No. 2.le-13;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRGSRPRRTSPRRRSKSPRRRSQSRESOC 34
   |||||
DB 150 rrrgrsrrrtsprrrrsksprrrrsqresqc 183

RESULT 4
AAR98879
ID AAR98879 standard; protein; 183 AA.
XX
AC AAR98879;
XX
DT 29-AUG-1996 (first entry)
XX
DE Hepatitis B virus E antigen mut4 (Lys74, Leu75) mutein.
XX
KW HBV; hepatitis B virus; antigen; HBeAg; specificity; diagnosis;
XX cross-reactivity; mutein; variant; modified.
XX
OS Hepatitis B virus.
XX Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 74..75
FT /note= "wild-type Ser74 and Asn75 have been
FT replaced by Lys74 and Leu75"
XX
PN JP08027185-A.
XX
PD 30-JAN-1996.
XX
PF 11-JUL-1994; 94JP-0180445.
XX
PR 11-JUL-1994; 94JP-0180445.
XX
PA (FJRE ) FUJI REBIO KK.
XX
DR WPI; 1996-136327/14.
XX
PN Novel anti-hepatitis-B-virus-e-antigen mutant for immuno:diagnosis
XX of hepatitis B - reacts specifically with anti-HBV-e-Ag antibody
XX without reacting with anti-HBV-c-Ag antibody
XX
PS Disclosure; Page -: 7pp; Japanese.
XX
CC The wild-type e-antigen of hepatitis B virus is recognised both by
XX anti-HBeAg antibodies and by anti-HBcAg antibodies. To increase the
XX sensitivity of immunodiagnosis of hepatitis B, at least one of
XX residues 74 or 75 of the wild-type e-antigen is mutated. The
XX mutations result in antigens having reduced reactivity with anti-
XX HBcAg antibodies (HBcAb) but which are still recognised by anti-
XX HBcAg antibodies (HBeAb). The present sequence is that of the mut4 mutein
XX which does not react at all with anti-HBcAb and reacts well with anti-
XX HBeAb (though not as well as wild-type HBeAg).
XX
SQ Sequence 183 AA;

Query Match      100.0%; Score 176; DB 17; Length 183;
Best Local Similarity 100.0%; Pred. No. 2.le-13;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRGSRPRRTSPRRRSKSPRRRSQSRESOC 34
   |||||
DB 150 rrrgrsrrrtsprrrrsksprrrrsqresqc 183

RESULT 5
AAR98881
ID AAR98881 standard; protein; 183 AA.
XX
AC AAR98881;
XX
DT 29-AUG-1996 (first entry)
XX
DE Hepatitis B virus E antigen mut28 (Ser74, Leu75) mutein.
XX
KW HBV; hepatitis B virus; antigen; HBeAg; specificity; diagnosis;
XX cross-reactivity; mutein; variant; modified.
XX

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AAR98880
ID AAR98880 standard; protein; 183 AA.
XX
AC AAR98880;
XX
DT 29-AUG-1996 (first entry)
XX
DE Hepatitis B virus E antigen mut27 (Asn74, Pro75) mutein.
XX
KW HBV; hepatitis B virus; antigen; HBeAg; specificity; diagnosis;
XX cross-reactivity; mutein; variant; modified.
XX
OS Hepatitis B virus.
XX Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 74..75
FT /note= "wild-type Ser74 and Asn75 have been
FT replaced by Asn74 and Pro75"
XX
PN JP08027185-A.
XX
PD 30-JAN-1996.
XX
PF 11-JUL-1994; 94JP-0180445.
XX
PR 11-JUL-1994; 94JP-0180445.
XX
PA (FJRE ) FUJI REBIO KK.
XX
DR WPI; 1996-136327/14.
XX
PN Novel anti-hepatitis-B-virus-e-antigen mutant for immuno:diagnosis
XX of hepatitis B - reacts specifically with anti-HBV-e-Ag antibody
XX without reacting with anti-HBV-c-Ag antibody
XX
PS Disclosure; Page -: 7pp; Japanese.
XX
CC The wild-type e-antigen of hepatitis B virus is recognised both by
XX anti-HBeAg antibodies and by anti-HBcAg antibodies. To increase the
XX sensitivity of immunodiagnosis of hepatitis B, at least one of
XX residues 74 or 75 of the wild-type e-antigen is mutated. The
XX mutations result in antigens having reduced reactivity with anti-
XX HBcAg antibodies (HBcAb) but which are still recognised by anti-
XX HBcAg antibodies (HBeAb). The present sequence is that of the mut27 mutein
XX which does not react at all with anti-HBcAb and reacts well with anti-
XX HBeAb (though not as well as wild-type HBeAg).
XX
SQ Sequence 183 AA;

Query Match      100.0%; Score 176; DB 17; Length 183;
Best Local Similarity 100.0%; Pred. No. 2.le-13;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRGSRPRRTSPRRRSKSPRRRSQSRESOC 34
   |||||
DB 150 rrrgrsrrrtsprrrrsksprrrrsqresqc 183

RESULT 6
AAR98881
ID AAR98881 standard; protein; 183 AA.
XX
AC AAR98881;
XX
DT 29-AUG-1996 (first entry)
XX
DE Hepatitis B virus E antigen mut28 (Ser74, Leu75) mutein.
XX
KW HBV; hepatitis B virus; antigen; HBeAg; specificity; diagnosis;
XX cross-reactivity; mutein; variant; modified.
XX

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RESULT 11  
 AAW33690  
 ID AAW33690 standard; Protein; 191 AA.  
 XX  
 AC AAW33690;  
 XX  
 DT 30-APR-1998 (first entry)  
 XX  
 DE Recombinant protein 150NA.  
 XX  
 KW Nucleic acid-binding motif; HCV; HBV; Hepatitis C virus; diagnosis;  
 KW core polypeptide; immunoassay; detection; antigen; disease; infection;  
 KW Hepatitis B virus; recombinant.  
 XX  
 OS Synthetic.  
 OS Chimeric - Hepatitis C virus.  
 OS Chimeric - Hepatitis B virus.  
 XX  
 PN EP805160-A1.  
 XX  
 PD 05-NOV-1997.  
 XX  
 PF 30-APR-1997; 97EP-0400985.  
 XX  
 PR 01-MAY-1996; 96JP-0134444.  
 XX  
 PA (FJRE ) FUJIREBIO INC.  
 XX  
 PI Itoh S, Takemura F, Ueno E;  
 XX  
 DR WPI; 1997-529030/49.  
 DR N-PSDB; AAV06338.  
 XX  
 PT Nucleic acid-bound polypeptide - useful as immunoassay reagent  
 XX  
 PS Example 1; Pages 22-23; 38pp; English.  
 CC This is a recombinant protein 150NA. This recombinant protein contains  
 CC the Hepatitis C virus (HCV) core polypeptide 150 fused to a nucleic  
 CC acid-binding motif present in the HBC protein of Hepatitis B virus  
 CC (HBV). This recombinant protein can be bound to a nucleic acid in the  
 CC host for producing a nucleic acid-bound polypeptide by a new method.  
 CC The method comprises producing a fusion gene containing the polypeptide  
 CC and the nucleic acid-binding motif, binding a nucleic acid to the  
 CC polypeptide as a soluble fraction, and purifying the nucleic acid-bound  
 CC polypeptide from the soluble fraction. When the polypeptide is a  
 CC recombinant form of an antigen, the nucleic acid-bound polypeptide can be  
 CC used as an immunoassay reagent for detecting the antigen or an antibody  
 CC to the antigen, especially in an agglutination assay using particles  
 CC coated with the nucleic acid-bound polypeptide. The methods can be  
 CC applied to diagnosis of disease and infection, especially for the  
 CC detection of HBV and HCV polypeptides. The nucleic acid-bound  
 CC polypeptides may be immunoreactive in cases where the free polypeptide  
 CC is not.  
 XX  
 SQ Sequence 191 AA;  
 Query Match 100.0%; Score 176; DB 18; Length 191;  
 Best Local Similarity 100.0%; Pred. No. 2.2e-13;  
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 RRGSRPRRTTSPRRRSKSPRRRSQSQ 34  
 Db 158 rrrgsprrrtsprrrrsksprrrsqrsq 191  
 RESULT 12  
 AAW33691  
 ID AAW33691 standard; Protein; 281 AA.  
 XX  
 AC AAW33691;  
 XX

DT 30-APR-1998 (first entry)  
 XX  
 DE Nucleic acid-bound polypeptide 120NA120.  
 XX  
 KW Nucleic acid-binding motif; HCV; HBV; Hepatitis C virus; diagnosis;  
 KW core polypeptide; immunoassay; detection; antigen; disease; infection;  
 KW Hepatitis B virus; recombinant.  
 XX  
 OS Synthetic.  
 OS Chimeric - Hepatitis C virus.  
 OS Chimeric - Hepatitis B virus.  
 XX  
 PN EP805160-A1.  
 XX  
 PD 05-NOV-1997.  
 XX  
 PF 30-APR-1997; 97EP-0400985.  
 XX  
 PR 01-MAY-1996; 96JP-0134444.  
 XX  
 PA (FJRE ) FUJIREBIO INC.  
 XX  
 PI Itoh S, Takemura F, Ueno E;  
 XX  
 DR WPI; 1997-529030/49.  
 DR N-PSDB; AAV06339.  
 XX  
 PT Nucleic acid-bound polypeptide - useful as immunoassay reagent  
 XX  
 PS Example 8; Pages 24-25; 38pp; English.  
 CC This is a nucleic acid-bound polypeptide 120NA120. This contains the  
 CC Hepatitis C virus (HCV) core polypeptide 120 and a nucleic acid-binding  
 CC motif present in the HBC protein of Hepatitis B virus (HBV). This nucleic  
 CC acid-bound polypeptide can be produced by a new method. The method  
 CC comprises producing a fusion gene containing the polypeptide and the  
 CC nucleic acid-binding motif, binding a nucleic acid to the polypeptide as  
 CC a soluble fraction, and purifying the nucleic acid-bound polypeptide from  
 CC the soluble fraction. When the polypeptide is a recombinant form of an  
 CC antigen, the nucleic acid-bound polypeptide can be used as an immunoassay  
 CC reagent for detecting the antigen or an antibody to the antigen,  
 CC especially in an agglutination assay using particles coated with the  
 CC nucleic acid-bound polypeptide. The methods can be applied to diagnosis  
 CC of disease and infection, especially for the detection of HBV and HCV  
 CC polypeptides. The nucleic acid-bound polypeptides may be immunoreactive  
 CC in cases where the free polypeptide is not.  
 XX  
 SQ Sequence 281 AA;  
 Query Match 100.0%; Score 176; DB 18; Length 281;  
 Best Local Similarity 100.0%; Pred. No. 3.2e-13;  
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 RRGSRPRRTTSPRRRSKSPRRRSQSQ 34  
 Db 126 rrrgsprrrtsprrrrsksprrrsqrsq 159  
 RESULT 13  
 AAW33693  
 ID AAW33693 standard; Protein; 456 AA.  
 XX  
 AC AAW33693;  
 XX  
 DT 30-APR-1998 (first entry)  
 XX  
 DE Nucleic acid-bound polypeptide TP47C2NA.  
 XX  
 KW Nucleic acid-binding motif; HCV; HBV; Hepatitis C virus; diagnosis;  
 KW core polypeptide; immunoassay; detection; antigen; disease; infection;  
 KW Hepatitis B virus; Treponema pallidum.  
 XX

OS Synthetic.  
OS Chimeric - Treponema pallidum.  
OS Chimeric - Hepatitis B virus.  
XX  
XX  
XX EP805160-A1.  
XX  
XX  
XX 05-NOV-1997.  
XX  
XX 30-APR-1997; 97EP-0400985.  
XX  
XX 01-MAY-1996; 96JP-0134444.  
XX  
XX (FJRE ) FUJIREBIO INC.  
XX

PI Itoh S, Takemura F, Ueno E;  
XX WPI; 1997-529030/49.  
XX N-PSDB; AAV06341.  
XX  
XX Nucleic acid-bound polypeptide - useful as immunoassay reagent  
XX  
XX Example 12; Pages 30-31; 38pp; English.  
XX  
XX This is a nucleic acid-bound polypeptide TP47C2NA. This contains the  
XX Treponema pallidum 47 kDa antigen and a nucleic acid-binding motif  
XX present in the Hbc protein of Hepatitis B virus (HBV). This nucleic  
XX acid-bound polypeptide can be produced by a new method. The method  
XX comprises producing a fusion gene containing the polypeptide and the  
XX nucleic acid-binding motif, binding a nucleic acid to the polypeptide as  
XX a soluble fraction, and purifying the nucleic acid-bound polypeptide from  
XX the soluble fraction. When the polypeptide is a recombinant form of an  
XX antigen, the nucleic acid-bound polypeptide can be used as an immunoassay  
XX reagent for detecting the antigen or an antibody to the antigen,  
XX especially in an agglutination assay using particles coated with the  
XX nucleic acid-bound polypeptide. The methods can be applied to diagnosis  
XX of disease and infection, especially for the detection of HBV and HCV  
XX polypeptides. The nucleic acid-bound polypeptides may be immunoreactive  
XX in cases where the free polypeptide is not.  
XX  
XX Sequence 456 AA;

Query Match 100.0%; Score 176; DB 18; Length 456;  
Best Local Similarity 100.0%; Pred. No. 4.9e-13;  
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 RRGSRPRRTTSPRRRSKSPRRRSQSRESQC 34  
DB 423 rrrgsprrrtsprrrrsksprrrrsqresqc 456

RESULT 14

AAFP00041  
ID AAP00041 standard; Protein; 183 AA.  
XX  
XX  
XX AAP00041;  
XX  
XX 14-OCT-1992 (first entry)  
XX  
XX Sequence of core antigen.  
XX  
XX Hepatitis B virus; antigen; antibody; diagnosis; vaccine.  
XX  
XX Hepatitis B virus.  
XX  
XX EP13828-A.  
XX  
XX 06-AUG-1980.  
XX  
XX 21-DEC-1979; 79EP-0303017.  
XX  
XX 01-NOV-1979; 79GB-0037910.  
XX  
XX 22-DEC-1978; 78GB-0049507.  
XX

PR 27-DEC-1978; 78GB-0050039.  
XX  
XX (BIOJ ) BIOGEN NV.  
XX  
XX Murray K, Schaller HE;  
XX  
XX WPI; 1980-57268C/33.  
XX  
XX N-PSDB; AAN00003.  
XX

XX Recombinant DNA coding for polypeptide - have specificity of  
XX hepatitis B viral antigens in detection or antibody stimulation  
XX  
XX Example; Flgs 3-4; 43pp; English.  
XX  
XX Human serum from a single HBsAg positive, HBeAg positive donor  
XX (serotype adym) was used to prep. a DNA-contg. pellet which was  
XX labelled with 3H or 32P as described by P. M. Kaplan et al (1973).  
XX The labelled DNA was then extracted with phenol from the resulting  
XX pellet using the procedure of L. I. Lutwick and W. S. Robinson (1977).  
XX It was then cloned in plasmid pBR322 which was used to transform E.  
XX coli. Micro-organisms prepd. by the processes are deposited at the  
XX NCIB as pBR322-HBV-G-L, e.g. E. coli HB101/pBR322-Pst I dg;  
XX HBV-Kpn I dc; Tetr AmpS HBV\*.  
XX  
XX Sequence 183 AA;

Query Match 97.7%; Score 172; DB 1; Length 183;  
Best Local Similarity 97.1%; Pred. No. 6.2e-13;  
Matches 33; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1 RRGSRPRRTTSPRRRSKSPRRRSQSRESQC 34  
DB 150 rrrgsprrrtsprrrrsksprrrrsqresqc 183

RESULT 15

AAFP40311  
ID AAP40311 standard; Protein; 183 AA.  
XX  
XX AAP40311;  
XX  
XX 18-AUG-1992 (first entry)  
XX  
XX Hepatitis virus core antigen.  
XX  
XX HBcAg; vaccine; diagnosis; HBV infection.  
XX  
XX Hepatitis b virus.  
XX  
XX JP59074985-A.  
XX  
XX 27-APR-1984.  
XX  
XX 19-OCT-1982; 82JP-0183432.  
XX  
XX 19-OCT-1982; 82JP-0183432.  
XX  
XX (TAKE ) TAKEDA CHEMICAL IND KK.  
XX  
XX WPI; 1984-143231/23.  
XX

XX DNA used in prevention of infections by hepatitis virus B -  
XX comprises structural gene of hepatitis virus adr B surface antigen  
XX coding gene and at least 1 virus core antigen structural gene.  
XX  
XX Disclosure; Fig 3; 13pp; Japanese.  
XX

XX The sequence is that of hepatitis virus core antigen (HBcAg). It  
XX can be used as a vaccine for the prevention of infections by  
XX hepatitis B virus (HBV) and also in the diagnosis of early stages  
XX of HBV infection. See also AAP40310.  
XX

50 Sequence 183 AA;

Query Match 97.7%; Score 172; DB 5; Length 183;  
 Best Local Similarity 97.1%; Pred. No. 6,2e-13;  
 Matches 33; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRGCSPPRRTPSPRRRSKSPRRRSQSRESQC 34  
 ||||||||||||||||||:|||||||||||  
 Db 150 rrrgrprrrtsprrrrsqprrrsqresgc 183

Search completed: April 18, 2002, 09:27:24  
 Job time: 32 sec



GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: April 18, 2002, 09:26:52 ; Search time 12.43 seconds  
(without alignments)  
61.554 Million cell updates/sec

Title: US-08-841-657A-2

Perfect score: 176

Sequence: 1 RRGGRSPRRTPSPRRRSKSPRRRSQSRESQC 34

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued\_Patents\_AA.\*

- 1: /cgn2\_6/ptodata/2/1aa/5A-COMB.pep.\*
- 2: /cgn2\_6/ptodata/2/1aa/5B-COMB.pep.\*
- 3: /cgn2\_6/ptodata/2/1aa/6A-COMB.pep.\*
- 4: /cgn2\_6/ptodata/2/1aa/6B-COMB.pep.\*
- 5: /cgn2\_6/ptodata/2/1aa/PCTUS-COMB.pep.\*
- 6: /cgn2\_6/ptodata/2/1aa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	172	97.7	39	US-08-968-747-5	Sequence 5, Appl
2	172	97.7	183	US-08-968-747-20	Sequence 20, Appl
3	172	97.7	183	US-09-248-588-2	Sequence 2, Appl
4	172	97.7	183	US-09-248-588-4	Sequence 4, Appl
5	172	97.7	193	US-08-968-747-2	Sequence 2, Appl
6	172	97.7	194	US-08-968-747-18	Sequence 18, Appl
7	172	97.7	199	US-08-968-747-21	Sequence 21, Appl
8	172	97.7	212	US-08-968-747-3	Sequence 3, Appl
9	172	97.7	346	US-08-105-483-217	Sequence 217, App
10	172	97.7	346	US-08-709-209-217	Sequence 217, App
11	172	97.7	346	US-08-458-101-217	Sequence 217, App
12	165	93.8	183	PCT-US96-10602-12	Sequence 12, Appl
13	165	93.8	185	US-07-739-642-2	Sequence 2, Appl
14	165	93.8	185	US-07-739-642-4	Sequence 4, Appl
15	165	93.8	185	US-07-739-642-8	Sequence 8, Appl
16	165	93.8	185	US-07-739-642-10	Sequence 10, Appl
17	165	93.8	185	US-07-739-643-2	Sequence 2, Appl
18	165	93.8	185	US-07-739-643-4	Sequence 4, Appl
19	165	93.8	185	US-07-739-643-8	Sequence 8, Appl
20	165	93.8	185	US-07-739-643-10	Sequence 10, Appl
21	165	93.8	185	US-07-739-142-2	Sequence 2, Appl
22	165	93.8	185	US-07-739-142-4	Sequence 4, Appl
23	165	93.8	185	US-07-739-142-8	Sequence 8, Appl
24	165	93.8	185	US-07-739-142-10	Sequence 10, Appl
25	165	93.8	185	US-09-248-588-6	Sequence 6, Appl
26	163	92.6	211	Patent No. 5196194-13	Patent No. 5196194
27	149	84.7	397	PCT-US96-10602-6	Sequence 6, Appl

28	141.5	80.4	217	4	US-09-248-588-9	Sequence 9, Appl
29	139.5	79.3	188	4	US-09-248-588-7	Sequence 7, Appl
30	136	77.3	289	5	PCT-US96-10602-8	Sequence 8, Appl
31	91	51.7	351	5	PCT-US96-10602-4	Sequence 4, Appl
32	87	49.4	345	5	PCT-US96-10602-2	Sequence 2, Appl
33	68	38.6	882	4	US-09-413-814-78	Sequence 78, Appl
34	67	38.1	140	2	US-08-557-309B-33	Sequence 33, Appl
35	67	38.1	140	3	US-08-834-306-33	Sequence 33, Appl
36	67	38.1	140	4	US-08-993-674A-33	Sequence 33, Appl
37	66	37.5	657	3	US-07-705-480-14	Sequence 14, Appl
38	66	37.5	657	4	US-07-751-891B-14	Sequence 14, Appl
39	65.5	37.2	432	2	US-08-933-750C-47	Sequence 47, Appl
40	65.5	37.2	432	4	US-09-234-613-47	Sequence 47, Appl
41	65	36.9	305	4	US-09-248-588-13	Sequence 13, Appl
42	64	36.4	301	2	US-08-656-906-25	Sequence 25, Appl
43	64	36.4	301	4	US-09-217-847-25	Sequence 25, Appl
44	64	36.4	614	5	PCT-US95-03236-21	Sequence 21, Appl
45	63	35.8	420	5	PCT-US96-10602-10	Sequence 10, Appl

## ALIGNMENTS

RESULT 1  
US-08-968-747-5  
; Sequence 5, Application US/08968747  
; Patent No. 6060595  
; GENERAL INFORMATION:  
; APPLICANT: Scaglioni et al.  
; TITLE OF INVENTION: INHIBITION OF VIRAL REPLICATION  
; NUMBER OF SEQUENCES: 21  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fish & Richardson P.C.  
; STREET: 225 Franklin Street  
; CITY: Boston  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02110-2804  
; COMPUTER READABLE FORM: disk  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: Windows  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/968,747  
; FILING DATE: 03-SEP-1997  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Fraser, Janis K.  
; REGISTRATION NUMBER: 34,819  
; REFERENCE/DOCKET NUMBER: 08472/705001  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 617/542-5070  
; TELEFAX: 617/542-8906  
; TELEX: 200154  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 39 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: not relevant  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-968-747-5

Query Match 97.7%; Score 172; DB 3; Length 39;  
Best Local Similarity 97.1%; Pred. No. 7.9e-15;  
Matches 33; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
OY 1 RRGGRSPRRTPSPRRRSKSPRRRSQSRESQC 34  
|||||  
Db 6 RRGGRSPRRTPSPRRRSKSPRRRSQSRESQC 39

RESULT 2  
US-08-968-747-20  
; Sequence 2, Application US/08968747  
; Patent No. 6060595  
; GENERAL INFORMATION:  
; APPLICANT: Scaglioni et al.  
; TITLE OF INVENTION: INHIBITION OF VIRAL REPLICATION  
; NUMBER OF SEQUENCES: 21  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fish & Richardson P.C.  
; STREET: 225 Franklin Street  
; CITY: Boston  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02110-2804  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: Windows  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION NUMBER: US/09/248,588  
; APPLICATION NUMBER: US/08/968,747  
; FILING DATE: 03-SEP-1997  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Fraser, Janis K.  
; REGISTRATION NUMBER: 34,819  
; REFERENCE/DOCKET NUMBER: 08472/705001  
; TELEPHONE: 617/542-5070  
; TELEFAX: 617/542-8906  
; TELEX: 200154  
; INFORMATION FOR SEQ ID NO: 20:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 183 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: not relevant  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-968-747-20

Query Match 97.7%; Score 172; DB 3; Length 183;  
Best Local Similarity 97.1%; Pred. No. 3.7e-14;  
Matches 33; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRGRSPRRTPSPRRRSKSPRRRSQSRESQC 34  
|||||  
DB 150 RRRGRSPRRTPSPRRRSQSRESQC 183

RESULT 3  
US-09-248-588-2  
; Sequence 2, Application US/09248588  
; Patent No. 6231864  
; GENERAL INFORMATION:  
; APPLICANT: Birkett, Ashley J.  
; TITLE OF INVENTION: Strategically Modified Hepatitis B Core Proteins and  
; FILE OF INVENTION: their Derivatives  
; FILE REFERENCE: SYN-101 4564/69529  
; CURRENT APPLICATION NUMBER: US/09/248,588  
; CURRENT FILING DATE: 1999-02-11  
; EARLIER APPLICATION NUMBER: 60/074537  
; FILING DATE: 1998-02-12  
; NUMBER OF SEQ ID NOS: 113  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 2  
; LENGTH: 183  
; TYPE: PRT  
; ORGANISM: Hepatitis B virus  
US-09-248-588-2

Query Match 97.7%; Score 172; DB 4; Length 183;  
Best Local Similarity 97.1%; Pred. No. 3.7e-14;  
Matches 33; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRGRSPRRTPSPRRRSKSPRRRSQSRESQC 34  
|||||  
DB 150 RRRGRSPRRTPSPRRRSQSRESQC 183

RESULT 4  
US-09-248-588-4  
; Sequence 4, Application US/09248588  
; Patent No. 6231864  
; GENERAL INFORMATION:  
; APPLICANT: Birkett, Ashley J.  
; TITLE OF INVENTION: Strategically Modified Hepatitis B Core Proteins and  
; FILE OF INVENTION: their Derivatives  
; FILE REFERENCE: SYN-101 4564/69529  
; CURRENT APPLICATION NUMBER: US/09/248,588  
; CURRENT FILING DATE: 1999-02-11  
; EARLIER APPLICATION NUMBER: 60/074537  
; FILING DATE: 1998-02-12  
; NUMBER OF SEQ ID NOS: 113  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 4  
; LENGTH: 183  
; TYPE: PRT  
; ORGANISM: Hepatitis B virus  
US-09-248-588-4

Query Match 97.7%; Score 172; DB 4; Length 183;  
Best Local Similarity 97.1%; Pred. No. 3.7e-14;  
Matches 33; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRGRSPRRTPSPRRRSKSPRRRSQSRESQC 34  
|||||  
DB 150 RRRGRSPRRTPSPRRRSQSRESQC 183

RESULT 5  
US-08-968-747-2  
; Sequence 2, Application US/08968747  
; Patent No. 6060595  
; GENERAL INFORMATION:  
; APPLICANT: Scaglioni et al.  
; TITLE OF INVENTION: INHIBITION OF VIRAL REPLICATION  
; NUMBER OF SEQUENCES: 21  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fish & Richardson P.C.  
; STREET: 225 Franklin Street  
; CITY: Boston  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02110-2804  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: Windows  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION NUMBER: US/08/968,747  
; FILING DATE: 03-SEP-1997  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Fraser, Janis K.  
; REGISTRATION NUMBER: 34,819  
; REFERENCE/DOCKET NUMBER: 08472/705001  
; TELEPHONE: 617/542-5070  
; TELEFAX: 617/542-8906  
; TELEX: 200154

INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 193 amino acids  
TYPE: amino acid  
STRANDEDNESS: not relevant  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-968-747-2

Query Match 97.7%; Score 172; DB 3; Length 193;  
Best Local Similarity 97.1%; Pred. No. 3.9e-14;  
Matches 33; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRGSRPRRTTSPRRRSQSPRRRSQSQSQ 34  
DB 160 RRGSRPRRTTSPRRRSQSPRRRSQSQSQ 193

## RESULT 6

US-08-968-747-18  
Sequence 18, Application US/08968747  
Patent No. 6060595

GENERAL INFORMATION:  
APPLICANT: Scaglioni et al.  
TITLE OF INVENTION: INHIBITION OF VIRAL REPLICATION  
NUMBER OF SEQUENCES: 21  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson P.C.  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02110-2804

COMPUTER READABLE FORM:  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: Windows  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/968,747  
FILING DATE: 03-SEP-1997  
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:  
NAME: Fraser, Janis K.  
REGISTRATION NUMBER: 34,819  
REFERENCE/DOCKET NUMBER: 08472/705001  
TELEPHONE: 617/542-5070  
TELEFAX: 617/542-8906  
TELEX: 200154

INFORMATION FOR SEQ ID NO: 18:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 194 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-968-747-18

Query Match 97.7%; Score 172; DB 3; Length 194;  
Best Local Similarity 97.1%; Pred. No. 3.9e-14;  
Matches 33; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRGSRPRRTTSPRRRSQSPRRRSQSQSQ 34  
DB 161 RRGSRPRRTTSPRRRSQSPRRRSQSQSQ 194

## RESULT 7

US-08-968-747-21  
Sequence 21, Application US/08968747  
Patent No. 6060595

GENERAL INFORMATION:  
APPLICANT: Scaglioni et al.  
TITLE OF INVENTION: INHIBITION OF VIRAL REPLICATION  
NUMBER OF SEQUENCES: 21  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson P.C.  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02110-2804

COMPUTER READABLE FORM:  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: Windows  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/968,747  
FILING DATE: 03-SEP-1997  
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:  
NAME: Fraser, Janis K.  
REGISTRATION NUMBER: 34,819  
REFERENCE/DOCKET NUMBER: 08472/705001  
TELEPHONE: 617/542-5070  
TELEFAX: 617/542-8906  
TELEX: 200154

INFORMATION FOR SEQ ID NO: 21:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 199 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-968-747-21

Query Match 97.7%; Score 172; DB 3; Length 199;  
Best Local Similarity 97.1%; Pred. No. 4e-14;  
Matches 33; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRGSRPRRTTSPRRRSQSPRRRSQSQSQ 34  
DB 166 RRGSRPRRTTSPRRRSQSPRRRSQSQSQ 199

## RESULT 8

US-08-968-747-3  
Sequence 3, Application US/08968747  
Patent No. 6060595

GENERAL INFORMATION:  
APPLICANT: Scaglioni et al.  
TITLE OF INVENTION: INHIBITION OF VIRAL REPLICATION  
NUMBER OF SEQUENCES: 21  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson P.C.  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02110-2804

COMPUTER READABLE FORM:  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: Windows  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/968,747  
FILING DATE: 03-SEP-1997  
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:  
NAME: Fraser, Janis K.  
REGISTRATION NUMBER: 34,819  
REFERENCE/DOCKET NUMBER: 08472/705001  
TELEPHONE: 617/542-5070  
TELEFAX: 617/542-8906  
TELEX: 200154

INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 199 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-968-747-21

Query Match 97.7%; Score 172; DB 3; Length 199;  
Best Local Similarity 97.1%; Pred. No. 4e-14;  
Matches 33; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRGSRPRRTTSPRRRSQSPRRRSQSQSQ 34  
DB 166 RRGSRPRRTTSPRRRSQSPRRRSQSQSQ 199

REFERENCE/DOCKET NUMBER: 08472/705001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617/542-5070  
TELEFAX: 617/542-8906  
TELEX: 200154

INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 212 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-968-747-3

Query Match 97.7%; Score 172; DB 3; Length 212;  
Best Local Similarity 97.1%; Pred. No. 4.3e-14;  
Matches 33; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRGSPRRTPSPRRRSQSPRRRSQSQ 34  
DB 179 RRRGSPRRTPSPRRRSQSPRRRSQSQ 212

## RESULT 9

US-08-105-483-217  
Sequence 217, Application US/08105483  
Patent No. 5494807

GENERAL INFORMATION:  
APPLICANT: Paoletti, Enzo  
TITLE OF INVENTION: GENETICALLY ENGINEERED VACCINE  
TITLE OF INVENTION: STRAIN  
NUMBER OF SEQUENCES: 462  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Curtis, Morris & Safford  
ADDRESSEE: c/o William S. Frommer  
STREET: 530 Fifth Avenue  
CITY: New York  
STATE: NY  
COUNTRY: USA  
ZIP: 10036

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/105,483  
FILING DATE: 12-AUG-1993  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/847,951  
FILING DATE: 06-MAR-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Frommer, William S.  
REGISTRATION NUMBER: 25,506  
REFERENCE/DOCKET NUMBER: 454310-2400

TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 840-3333  
TELEFAX: (212) 840-0712  
INFORMATION FOR SEQ ID NO: 217:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 346 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-105-483-217

Query Match 97.7%; Score 172; DB 1; Length 346;  
Best Local Similarity 97.1%; Pred. No. 7e-14;  
Matches 33; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRGSPRRTPSPRRRSQSPRRRSQSQ 34

DB 313 RRRGSPRRTPSPRRRSQSPRRRSQSQ 346

## RESULT 10

US-08-709-209-217  
Sequence 217, Application US/08709209  
Patent No. 5762938  
GENERAL INFORMATION:  
APPLICANT: Paoletti, Enzo  
TITLE OF INVENTION: GENETICALLY ENGINEERED VACCINE  
TITLE OF INVENTION: STRAIN  
NUMBER OF SEQUENCES: 462  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Curtis, Morris & Safford  
ADDRESSEE: c/o William S. Frommer  
STREET: 530 Fifth Avenue  
CITY: New York  
STATE: NY  
COUNTRY: USA  
ZIP: 10036

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/709,209  
FILING DATE: 21-AUG-1996  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/105,483  
FILING DATE: 12-AUG-1993  
APPLICATION NUMBER: US 07/847,951  
FILING DATE: 06-MAR-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Frommer, William S.  
REGISTRATION NUMBER: 25,506  
REFERENCE/DOCKET NUMBER: 454310-2400  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 840-3333  
TELEFAX: (212) 840-0712  
INFORMATION FOR SEQ ID NO: 217:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 346 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-709-209-217

Query Match 97.7%; Score 172; DB 1; Length 346;  
Best Local Similarity 97.1%; Pred. No. 7e-14;  
Matches 33; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRGSPRRTPSPRRRSQSPRRRSQSQ 34  
DB 313 RRRGSPRRTPSPRRRSQSPRRRSQSQ 346

## RESULT 11

US-08-458-101-217  
Sequence 217, Application US/08458101  
Patent No. 5766599  
GENERAL INFORMATION:  
APPLICANT: Paoletti, Enzo  
APPLICANT: Perkus, Marion E.  
APPLICANT: Taylor, Jill  
APPLICANT: Tartaglia, James  
APPLICANT: No. 5766599ton, Elizabeth K.  
APPLICANT: Riviere, Michel  
APPLICANT: de Taisne, Charles  
APPLICANT: Limbach, Keith J.

APPLICANT: Johnson, Gerard P.  
APPLICANT: Pincus, Steven E.  
APPLICANT: Cox, William I.  
APPLICANT: Audonnet, Jean-Christophe Francis  
APPLICANT: Gettig, Russell Robert  
TITLE OF INVENTION: GENETICALLY ENGINEERED VACCINE  
TITLE OF INVENTION: STRAIN  
NUMBER OF SEQUENCES: 467  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Curtis, Morris & Safford  
ADDRESSEE: c/o William S. Frommer  
STREET: 530 Fifth Avenue  
CITY: New York  
STATE: NY  
COUNTRY: USA  
ZIP: 10036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/458.101  
FILING DATE: 01-JUN-1995  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Frommer, William S.  
REGISTRATION NUMBER: 25,506  
REFERENCE/DOCKET NUMBER: 454310-2740  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 840-3333  
TELEFAX: (212) 840-0712  
INFORMATION FOR SEQ ID NO: 217:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 346 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-458-101-217

Query Match 97.7%; Score 172; DB 1; Length 346;  
Best Local Similarity 97.1%; Pred. No. 7e-14;  
Matches 33; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRGSRPRRTSPRRRSKSPRRRSQSRESQC 34  
|||||  
DB 313 RRGSRPRRTSPRRRSKSPRRRSQSRESQC 346

RESULT 12  
PCT-US96-10602-12  
Sequence 12, Application PC/TUS9610602  
GENERAL INFORMATION:  
APPLICANT: The General Hospital Corporation  
TITLE OF INVENTION: INHIBITION OF HEPATITIS B REPLICATION  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson P.C.  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02110-2804  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US96/10602  
FILING DATE:  
CLASSIFICATION:

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/017,814  
FILING DATE: 20-JUN-1995  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Clark, Paul T.  
REGISTRATION NUMBER: 30,162  
REFERENCE/DOCKET NUMBER: 00786/282001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617/542-5070  
TELEFAX: 617/542-8906  
TELEX: 200154  
INFORMATION FOR SEQ ID NO: 12:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 183 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
PCT-US96-10602-12

Query Match 93.8%; Score 165; DB 5; Length 183;  
Best Local Similarity 94.1%; Pred. No. 2.6e-13;  
Matches 32; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RRGSRPRRTSPRRRSKSPRRRSQSRESQC 34  
|||||  
DB 150 RRGSRPRRTSPRRRSKSPRRRSQSRESQC 183

RESULT 13  
US-07-739-642-2  
Sequence 2, Application US/07739642  
Patent No. 5173427  
GENERAL INFORMATION:  
APPLICANT: Mallonee, Richard L.  
TITLE OF INVENTION: Vectors And Hosts With Increased  
Expression Of HBCag  
NUMBER OF SEQUENCES: 24  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Richard R. Rodrick  
STREET: 1 Becton Drive  
CITY: Franklin Lakes  
STATE: New Jersey  
COUNTRY: U.S.A.  
ZIP: 07417-1880  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/739,642  
FILING DATE: 19910801  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Stierwalt, Brian K.  
REGISTRATION NUMBER: 33,213  
REFERENCE/DOCKET NUMBER: P-2272  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 201-848-5317  
TELEFAX: 201-848-9228  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 185 amino acids  
TYPE: AMINO ACID  
TOPOLOGY: linear  
US-07-739-642-2

Query Match 93.8%; Score 165; DB 1; Length 185;  
Best Local Similarity 94.1%; Pred. No. 2.6e-13;  
Matches 32; Conservative 1; Mismatches 1; Indels 0; Gaps 0;



Thu Apr 18 10:44:57 2002

us-08-841-657a-2.ra1

Page 7

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: April 18, 2002, 09:36:52 ; Search time 10.17 Seconds  
(without alignments)  
122.577 Million cell updates/sec

Title: US-08-841-657a-2

Perfect score: 176

Sequence: 1 RRGSRPRRTSPRRRSKSPRRRSQSRESQC 34

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 100059 seqs, 36664827 residues

Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_39.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Query Match	Score	Length	ID	Description
1	172	97.7	183	1	CORA_HPBV4
2	172	97.7	183	1	CORA_HPBVJ
3	172	97.7	183	1	CORA_HPBVO
4	172	97.7	183	1	CORA_HPBVY
5	172	97.7	183	1	CORA_HPBVZ
6	170	96.6	195	1	CORA_HPBVF
7	169	96.0	211	1	CORA_HPBVA
8	165	93.8	214	1	CORA_HPBVA
9	165	93.8	214	1	CORA_HPBVA
10	159	90.3	212	1	CORA_HPBVL
11	159	90.3	212	1	CORA_HPBVL
12	158	89.8	185	1	CORA_HPBVT
13	141.5	80.4	217	1	CORA_HPBVG
14	139.5	79.3	188	1	CORA_HPBVS
15	135	76.7	187	1	CORA_HPBV8
16	105	59.7	196	1	SFR2_HUMAN
17	98.5	56.0	484	1	SFR2_HUMAN
18	95.5	54.3	208	1	YSX2_CAEEL
19	82	46.6	77	1	PRR2_SEPOF
20	76.5	43.5	951	1	HSP1_HUMAN
21	76	43.2	61	1	HSP1_HACEU
22	76	43.2	1634	1	PCFB_HUMAN
23	75	42.6	221	1	SFR2_CHICK
24	75	42.6	221	1	SFR2_HUMAN
25	75	42.6	221	1	SFR2_MOUSE
26	74.5	42.3	78	1	PR11_SEPOF
27	74.5	42.3	739	1	DD15_CAEEL
28	73.5	41.8	1523	1	SON_HUMAN
29	73	41.5	60	1	HSP1_WACGI
30	73	41.5	61	1	HSP1_WACRG
31	72.5	41.2	303	1	SFR1_ARATH
32	72	40.9	483	1	VE2_HPV14
33	72	40.9	503	1	VE2_HPV21

34 71.5 40.6 91 1 PHIL\_MYTED  
35 71 40.3 57 1 HSP1\_DIDMA  
36 71 40.3 61 1 HSP\_CHICK  
37 71 40.3 164 1 SFR3\_HUMAN  
38 71 40.3 356 1 RS41\_ARATH  
39 70.5 40.1 498 1 VE2\_HPV08  
40 69 39.2 238 1 SFR7\_HUMAN  
41 69 39.2 1200 1 DD18\_CAEEL  
42 68 38.6 305 1 CORA\_HPBDC  
43 68 38.6 350 1 RS40\_ARATH  
44 68 38.6 350 1 RS40\_ARATH  
45 68 38.6 1042 1 SUWA\_DROME

## ALIGNMENTS

RESULT 1  
CORA\_HPBV4  
ID CORA\_HPBV4 STANDARD; PRT; 183 AA.  
AC P03150; P03151;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 01-FEB-1991 (Rel. 17, Last annotation update)  
DE CORE ANTIGEN.  
GN C.  
OS Hepatitis B virus (subtype adr4), Hepatitis B virus (subtype adr), and  
OS Hepatitis B virus (subtype adr / strain Indonesia/p1DM420).  
OC Viruses; Retroviridae; Hepadnaviridae; Orthohepadnavirus.  
OX NCBI\_TaxID=10409, 106820, 10412;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=ADR;  
RX MEDLINE=83168919; PubMed=6300776;  
RA Ono Y., Onda H., Sasada R., Igarashi K., Sugino Y., Nishioka K.;  
RT "The complete nucleotide sequences of the cloned Hepatitis B virus  
RL DNA; subtype adr and adr4";  
RL Nucleic Acids Res. 11:1747-1757 (1983).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=ADR4;  
RX MEDLINE=83246570; PubMed=6306594;  
RA Fujiyama A., Miyano H., Yoneyama T., Ohtomo N.,  
RA Matsubara K.;  
RT "Cloning and structural analyses of hepatitis B virus DNAs, subtype  
RL adr";  
RL Nucleic Acids Res. 11:4601-4610 (1983).  
RN [3]  
RP SEQUENCE FROM N.A.  
RC STRAIN=ADW;  
RX MEDLINE=89010694; PubMed=3171552;  
RA Okamoto H., Tsuda F., Sakugawa H., Sastrosowigno R.I., Imai M.,  
RA Miyakawa Y., Mayumi M.;  
RT "Typing hepatitis B virus by homology in nucleotide sequence:  
RL comparison of surface antigen subtypes";  
RL J. Gen. Virol. 69:2575-2583 (1988).  
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CC  
CC EMBL: V00867; ; NOT\_ANNOTATED\_CDS.  
DR EMBL: X01587; CAA23745.1; ;  
DR EMBL: D00331; ; NOT\_ANNOTATED\_CDS.  
DR PIR: A33480; NKVLA5.  
DR PIR: B33460; NKVLA5.  
DR PIR: C28925; NKVLA3.  
DR InterPro: IPR002006; Hepatitis\_core.  
DR Pfam: PF00906; Hepatitis\_core; 1.



KW Core protein; Repeat.  
 FT REPEAT 162 169  
 FT REPEAT 170 177  
 SQ SEQUENCE 183 AA; 21095 MW; ED2DA1DB07FB596D CRC64;

Query Match 97.7%; Score 172; DB 1; Length 183;  
 Best Local Similarity 97.1%; Pred. No. 1.9e-12;  
 Matches 33; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 RRRGSRPRRTSPRRRSKSPRRRSQSRESQC 34  
 |||||  
 DB 150 RRRGSRPRRTSPRRRSKSPRRRSQSRESQC 183

## RESULT 2

CORA\_HPBVJ STANDARD; PRT; 183 AA.  
 AC P17391;  
 DT 01-AUG-1990 (Rel. 15, Created)  
 DT 01-AUG-1990 (Rel. 15, Last sequence update)  
 DT 01-FEB-1991 (Rel. 17, Last annotation update)  
 DE CORE ANTIGEN.  
 OS Hepatitis B virus (subtype adv / strain Japan/pjdw233).  
 OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.  
 OX NCBI\_TaxID=10413;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=89010694; PubMed=3171552;  
 RA Okamoto H., Tsuda F., Sakagawa H., Sastroewignjo R.I., Imai M.,  
 RA Miyakawa Y., Mayumi M.;  
 RT "Typing hepatitis B virus by homology in nucleotide sequence:  
 RT comparison of surface antigen subtypes.";  
 RL J. Gen. Virol. 69:2575-2583(1988).  
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 DR EMBL; D00329; -; NOT\_ANNOTATED\_CDS.  
 DR PIR; A28925; NKVLJ1.  
 DR InterPro; IPR002006; Hepatitis\_core.  
 DR Pfam; PF00906; Hepatitis\_core; 1.  
 KW Core protein; Repeat.  
 FT REPEAT 162 169  
 FT REPEAT 170 177  
 SQ SEQUENCE 183 AA; 21224 MW; 9FDD6B5F5AF5E160 CRC64;

Query Match 97.7%; Score 172; DB 1; Length 183;  
 Best Local Similarity 97.1%; Pred. No. 1.9e-12;  
 Matches 33; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 RRRGSRPRRTSPRRRSKSPRRRSQSRESQC 34  
 |||||  
 DB 150 RRRGSRPRRTSPRRRSKSPRRRSQSRESQC 183

## RESULT 3

CORA\_HPBVJ STANDARD; PRT; 183 AA.  
 AC P17392;  
 DT 01-AUG-1990 (Rel. 15, Created)  
 DT 01-AUG-1990 (Rel. 15, Last sequence update)  
 DT 01-FEB-1991 (Rel. 17, Last annotation update)  
 DE CORE ANTIGEN.  
 OS Hepatitis B virus (subtype adv / strain Okinawa/pjdw282).  
 OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.  
 OX NCBI\_TaxID=10415;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=89010694; PubMed=3171552;  
 RA Okamoto H., Tsuda F., Sakagawa H., Sastroewignjo R.I., Imai M.,  
 RA Miyakawa Y., Mayumi M.;  
 RT "Typing hepatitis B virus by homology in nucleotide sequence:  
 RT comparison of surface antigen subtypes.";  
 RL J. Gen. Virol. 69:2575-2583(1988).  
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 DR EMBL; D00329; -; NOT\_ANNOTATED\_CDS.  
 DR PIR; A28925; NKVLJ1.  
 DR InterPro; IPR002006; Hepatitis\_core.  
 DR Pfam; PF00906; Hepatitis\_core; 1.  
 KW Core protein; Repeat.  
 FT REPEAT 162 169  
 FT REPEAT 170 177  
 SQ SEQUENCE 183 AA; 21224 MW; 9FDD6B5F5AF5E160 CRC64;

RN SEQUENCE FROM N.A.  
 RX MEDLINE=89010694; PubMed=3171552;  
 RA Okamoto H., Tsuda F., Sakagawa H., Sastroewignjo R.I., Imai M.,  
 RA Miyakawa Y., Mayumi M.;  
 RT "Typing hepatitis B virus by homology in nucleotide sequence:  
 RT comparison of surface antigen subtypes.";  
 RL J. Gen. Virol. 69:2575-2583(1988).  
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 DR EMBL; D00330; -; NOT\_ANNOTATED\_CDS.  
 DR PIR; B28925; NKVLJ2.  
 DR InterPro; IPR002006; Hepatitis\_core.  
 DR Pfam; PF00906; Hepatitis\_core; 1.  
 KW Core protein; Repeat.  
 FT REPEAT 162 169  
 FT REPEAT 170 177  
 SQ SEQUENCE 183 AA; 21081 MW; 66BDB2633122930C CRC64;

Query Match 97.7%; Score 172; DB 1; Length 183;  
 Best Local Similarity 97.1%; Pred. No. 1.9e-12;  
 Matches 33; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 RRRGSRPRRTSPRRRSKSPRRRSQSRESQC 34  
 |||||  
 DB 150 RRRGSRPRRTSPRRRSKSPRRRSQSRESQC 183

RESULT 4  
 CORA\_HPBVJ STANDARD; PRT; 183 AA.  
 AC P03146;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 01-APR-1990 (Rel. 14, Last annotation update)  
 DE CORE ANTIGEN.  
 GN C.  
 OS Hepatitis B virus (subtype ayw).  
 OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.  
 OX NCBI\_TaxID=10418;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=81012091; PubMed=399327;  
 RA Gallibert F., Mandart E., Fitoussi F., Tiollais P., Charnay P.;  
 RT "Nucleotide sequence of the hepatitis B virus genome (subtype ayw)  
 RT cloned in E. coli.";  
 RL Nature 281:646-650(1979).  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 DR EMBL; V01450; CAA24706.1; ALT\_INIT.  
 DR EMBL; X02496; -; NOT\_ANNOTATED\_CDS.

Query Match 97.7%; Score 172; DB 1; Length 183;  
 Best Local Similarity 97.1%; Pred. No. 1.9e-12;  
 Matches 33; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 RRRGSRPRRTSPRRRSKSPRRRSQSRESQC 34  
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 DB 150 RRRGSRPRRTSPRRRSKSPRRRSQSRESQC 183

RESULT 4  
 CORA\_HPBVJ STANDARD; PRT; 183 AA.  
 AC P03146;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 01-APR-1990 (Rel. 14, Last annotation update)  
 DE CORE ANTIGEN.  
 GN C.  
 OS Hepatitis B virus (subtype ayw).  
 OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.  
 OX NCBI\_TaxID=10418;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=81012091; PubMed=399327;  
 RA Gallibert F., Mandart E., Fitoussi F., Tiollais P., Charnay P.;  
 RT "Nucleotide sequence of the hepatitis B virus genome (subtype ayw)  
 RT cloned in E. coli.";  
 RL Nature 281:646-650(1979).  
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 DR EMBL; V01450; CAA24706.1; ALT\_INIT.  
 DR EMBL; X02496; -; NOT\_ANNOTATED\_CDS.

Query Match 97.7%; Score 172; DB 1; Length 183;  
 Best Local Similarity 97.1%; Pred. No. 1.9e-12;  
 Matches 33; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 RRRGSRPRRTSPRRRSKSPRRRSQSRESQC 34  
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 DB 150 RRRGSRPRRTSPRRRSKSPRRRSQSRESQC 183

RESULT 4  
 CORA\_HPBVJ STANDARD; PRT; 183 AA.  
 AC P03146;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 01-APR-1990 (Rel. 14, Last annotation update)  
 DE CORE ANTIGEN.  
 GN C.  
 OS Hepatitis B virus (subtype ayw).  
 OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.  
 OX NCBI\_TaxID=10418;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=81012091; PubMed=399327;  
 RA Gallibert F., Mandart E., Fitoussi F., Tiollais P., Charnay P.;  
 RT "Nucleotide sequence of the hepatitis B virus genome (subtype ayw)  
 RT cloned in E. coli.";  
 RL Nature 281:646-650(1979).  
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 DR EMBL; V01450; CAA24706.1; ALT\_INIT.  
 DR EMBL; X02496; -; NOT\_ANNOTATED\_CDS.

Query Match 97.7%; Score 172; DB 1; Length 183;  
 Best Local Similarity 97.1%; Pred. No. 1.9e-12;  
 Matches 33; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 RRRGSRPRRTSPRRRSKSPRRRSQSRESQC 34  
 |||||  
 DB 150 RRRGSRPRRTSPRRRSKSPRRRSQSRESQC 183

RESULT 4  
 CORA\_HPBVJ STANDARD; PRT; 183 AA.  
 AC P03146;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 01-APR-1990 (Rel. 14, Last annotation update)  
 DE CORE ANTIGEN.  
 GN C.  
 OS Hepatitis B virus (subtype ayw).  
 OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.  
 OX NCBI\_TaxID=10418;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=81012091; PubMed=399327;  
 RA Gallibert F., Mandart E., Fitoussi F., Tiollais P., Charnay P.;  
 RT "Nucleotide sequence of the hepatitis B virus genome (subtype ayw)  
 RT cloned in E. coli.";  
 RL Nature 281:646-650(1979).  
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 DR EMBL; V01450; CAA24706.1; ALT\_INIT.  
 DR EMBL; X02496; -; NOT\_ANNOTATED\_CDS.

Query Match 97.7%; Score 172; DB 1; Length 183;  
 Best Local Similarity 97.1%; Pred. No. 1.9e-12;  
 Matches 33; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 RRRGSRPRRTSPRRRSKSPRRRSQSRESQC 34  
 |||||  
 DB 150 RRRGSRPRRTSPRRRSKSPRRRSQSRESQC 183

RESULT 4  
 CORA\_HPBVJ STANDARD; PRT; 183 AA.  
 AC P03146;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 01-APR-1990 (Rel. 14, Last annotation update)  
 DE CORE ANTIGEN.  
 GN C.  
 OS Hepatitis B virus (subtype ayw).  
 OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.  
 OX NCBI\_TaxID=10418;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=81012091; PubMed=399327;  
 RA Gallibert F., Mandart E., Fitoussi F., Tiollais P., Charnay P.;  
 RT "Nucleotide sequence of the hepatitis B virus genome (subtype ayw)  
 RT cloned in E. coli.";  
 RL Nature 281:646-650(1979).  
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 DR EMBL; V01450; CAA24706.1; ALT\_INIT.  
 DR EMBL; X02496; -; NOT\_ANNOTATED\_CDS.

Query Match 97.7%; Score 172; DB 1; Length 183;  
 Best Local Similarity 97.1%; Pred. No. 1.9e-12;  
 Matches 33; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 RRRGSRPRRTSPRRRSKSPRRRSQSRESQC 34  
 |||||  
 DB 150 RRRGSRPRRTSPRRRSKSPRRRSQSRESQC 183

RESULT 4  
 CORA\_HPBVJ STANDARD; PRT; 183 AA.  
 AC P03146;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 01-APR-1990 (Rel. 14, Last annotation update)  
 DE CORE ANTIGEN.  
 GN C.  
 OS Hepatitis B virus (subtype ayw).  
 OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.  
 OX NCBI\_TaxID=10418;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=81012091; PubMed=399327;  
 RA Gallibert F., Mandart E., Fitoussi F., Tiollais P., Charnay P.;  
 RT "Nucleotide sequence of the hepatitis B virus genome (subtype ayw)  
 RT cloned in E. coli.";  
 RL Nature 281:646-650(1979).  
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 DR EMBL; V01450; CAA24706.1; ALT\_INIT.  
 DR EMBL; X02496; -; NOT\_ANNOTATED\_CDS.

Query Match 97.7%; Score 172; DB 1; Length 183;  
 Best Local Similarity 97.1%; Pred. No. 1.9e-12;  
 Matches 33; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 RRRGSRPRRTSPRRRSKSPRRRSQSRESQC 34  
 |||||  
 DB 150 RRRGSRPRRTSPRRRSKSPRRRSQSRESQC 183

RESULT 4  
 CORA\_HPBVJ STANDARD; PRT; 183 AA.  
 AC P03146;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 01-APR-1990 (Rel. 14, Last annotation update)  
 DE CORE ANTIGEN.  
 GN C.  
 OS Hepatitis B virus (subtype ayw).  
 OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.  
 OX NCBI\_TaxID=10418;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=81012091; PubMed=399327;  
 RA Gallibert F., Mandart E., Fitoussi F., Tiollais P., Charnay P.;  
 RT "Nucleotide sequence of the hepatitis B virus genome (subtype ayw)  
 RT cloned in E. coli.";  
 RL Nature 281:646-650(1979).  
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 DR EMBL; V01450; CAA24706.1; ALT\_INIT.  
 DR EMBL; X02496; -; NOT\_ANNOTATED\_CDS.

DR PIR; A03711; NKVLAH.  
 DR PIR; A03712; NKVLBH.  
 DR InterPro: IPR002006; Hepatitis\_core.  
 DR Pfam: PF00906; Hepatitis\_core; 1.  
 KW Core protein; Repeat.  
 FT REPEAT 162 169  
 FT REPEAT 170 177  
 FT CONFLICT 33 33 T -> N (IN REF. 2).  
 FT CONFLICT 80 80 A -> I (IN REF. 2).  
 FT CONFLICT 80 80 A -> I (IN REF. 2).  
 SQ SEQUENCE 183 AA; 21116 MW; E0D9D9763F24E958 CRC64;

Query Match 97.7%; Score 172; DB 1; Length 183;  
 Best Local Similarity 97.1%; Pred. No. 1.9e-12;

Matches 33; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 RRGGRSPRRTPSPRRRSKSPRRRSQRESQC 34  
 DB 150 RRGGRSPRRTPSPRRRSKSPRRRSQRESQC 183

## RESULT 5

CORA\_HPBVZ STANDARD; PRT; 183 AA.

AC P03147; 1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 01-OCT-1989 (Rel. 12, Last annotation update)  
 DE CORE ANTIGEN.

GN CORE ANTIGEN.

OS Hepatitis B virus (subtype advw).  
 OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.  
 OX NCBI\_TaxID=10419;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=8102115; PubMed=399329;

RA Pask M., Goto T., Gilbert W., Zink B., Schaller H., McKay P.,

RA Leadbetter G., Murray K.,

RT "Hepatitis B virus genes and their expression in E. coli.";

RL Nature 282:575-579(1979).

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 CC -----

DR EMBL; J02202; AAA45486.1; -

DR EMBL; A08967; CAA00816.1; -

DR PIR; B93217; NKVL2.

DR InterPro: IPR002006; Hepatitis\_core.

DR Pfam; PF00906; Hepatitis\_core; 1.

KW Core protein; Repeat.

FT REPEAT 162 169

FT REPEAT 170 177

SQ SEQUENCE 183 AA; 21042 MW; 545ED0E5527F26C CRC64;

## Query Match

Best Local Similarity 97.7%; Score 172; DB 1; Length 183;

Matches 33; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 RRGGRSPRRTPSPRRRSKSPRRRSQRESQC 34  
 DB 150 RRGGRSPRRTPSPRRRSKSPRRRSQRESQC 183

## RESULT 6

CORA\_HPBVZ STANDARD; PRT; 195 AA.

AC P29178;

DT 01-DEC-1992 (Rel. 24, Created)  
 DT 01-DEC-1992 (Rel. 24, Last sequence update)  
 DT 01-DEC-1992 (Rel. 24, Last annotation update)  
 DE CORE ANTIGEN.

GN CORE ANTIGEN.

OS Hepatitis B virus (subtype adv2 variant sf).

OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.

OX NCBI\_TaxID=31515;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=9018950; PubMed=2307406;

RA Bhat R.A., Ulrich P.P., Vyas G.N.;

RT "Molecular characterization of a new variant of hepatitis B virus in

RT a persistently infected homosexual man.";

RL Hepatology 11:271-276(1990).

DR PIR; A37182; NKVLH3.

DR InterPro: IPR002006; Hepatitis\_core.

DR Pfam; PF00906; Hepatitis\_core; 1.

KW Core protein; Repeat.

FT REPEAT 174 181

FT REPEAT 182 189

SQ SEQUENCE 195 AA; 22461 MW; E2B166F879CB7CB7 CRC64;

Query Match 96.6%; Score 170; DB 1; Length 195;

Best Local Similarity 97.1%; Pred. No. 3.3e-12;

Matches 33; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 RRGGRSPRRTPSPRRRSKSPRRRSQRESQC 34

DB 162 RRGGRSPRRTPSPRRRSKSPRRRSQRESQC 195

DB 162 RRGGRSPRRTPSPRRRSKSPRRRSQRESQC 195

DB 162 RRGGRSPRRTPSPRRRSKSPRRRSQRESQC 195

DB 162 RRGGRSPRRTPSPRRRSKSPRRRSQRESQC 195

DB 162 RRGGRSPRRTPSPRRRSKSPRRRSQRESQC 195

DB 162 RRGGRSPRRTPSPRRRSKSPRRRSQRESQC 195

DB 162 RRGGRSPRRTPSPRRRSKSPRRRSQRESQC 195

DB 162 RRGGRSPRRTPSPRRRSKSPRRRSQRESQC 195

DB 162 RRGGRSPRRTPSPRRRSKSPRRRSQRESQC 195

DB 162 RRGGRSPRRTPSPRRRSKSPRRRSQRESQC 195

DB 162 RRGGRSPRRTPSPRRRSKSPRRRSQRESQC 195

DB 162 RRGGRSPRRTPSPRRRSKSPRRRSQRESQC 195

DB 162 RRGGRSPRRTPSPRRRSKSPRRRSQRESQC 195

DB 162 RRGGRSPRRTPSPRRRSKSPRRRSQRESQC 195

DB 162 RRGGRSPRRTPSPRRRSKSPRRRSQRESQC 195

DB 162 RRGGRSPRRTPSPRRRSKSPRRRSQRESQC 195

DB 162 RRGGRSPRRTPSPRRRSKSPRRRSQRESQC 195

DB 162 RRGGRSPRRTPSPRRRSKSPRRRSQRESQC 195

DB 162 RRGGRSPRRTPSPRRRSKSPRRRSQRESQC 195

DB 162 RRGGRSPRRTPSPRRRSKSPRRRSQRESQC 195

DB 162 RRGGRSPRRTPSPRRRSKSPRRRSQRESQC 195

DB 162 RRGGRSPRRTPSPRRRSKSPRRRSQRESQC 195

DB 162 RRGGRSPRRTPSPRRRSKSPRRRSQRESQC 195

DB 162 RRGGRSPRRTPSPRRRSKSPRRRSQRESQC 195

DB 162 RRGGRSPRRTPSPRRRSKSPRRRSQRESQC 195

DB 162 RRGGRSPRRTPSPRRRSKSPRRRSQRESQC 195

DB 162 RRGGRSPRRTPSPRRRSKSPRRRSQRESQC 195

DB 162 RRGGRSPRRTPSPRRRSKSPRRRSQRESQC 195

DB 162 RRGGRSPRRTPSPRRRSKSPRRRSQRESQC 195

DB 162 RRGGRSPRRTPSPRRRSKSPRRRSQRESQC 195

DB 162 RRGGRSPRRTPSPRRRSKSPRRRSQRESQC 195

DB 162 RRGGRSPRRTPSPRRRSKSPRRRSQRESQC 195

DB 162 RRGGRSPRRTPSPRRRSKSPRRRSQRESQC 195

DB 162 RRGGRSPRRTPSPRRRSKSPRRRSQRESQC 195

DB 162 RRGGRSPRRTPSPRRRSKSPRRRSQRESQC 195

DB 162 RRGGRSPRRTPSPRRRSKSPRRRSQRESQC 195

DB 162 RRGGRSPRRTPSPRRRSKSPRRRSQRESQC 195

DB 162 RRGGRSPRRTPSPRRRSKSPRRRSQRESQC 195

DB 162 RRGGRSPRRTPSPRRRSKSPRRRSQRESQC 195

DB 162 RRGGRSPRRTPSPRRRSKSPRRRSQRESQC 195

DB 162 RRGGRSPRRTPSPRRRSKSPRRRSQRESQC 195

DB 162 RRGGRSPRRTPSPRRRSKSPRRRSQRESQC 195

DB 162 RRGGRSPRRTPSPRRRSKSPRRRSQRESQC 195

DB 162 RRGGRSPRRTPSPRRRSKSPRRRSQRESQC 195

DB 162 RRGGRSPRRTPSPRRRSKSPRRRSQRESQC 195

DB 162 RRGGRSPRRTPSPRRRSKSPRRRSQRESQC 195

DB 162 RRGGRSPRRTPSPRRRSKSPRRRSQRESQC 195

DB 162 RRGGRSPRRTPSPRRRSKSPRRRSQRESQC 195

DB 162 RRGGRSPRRTPSPRRRSKSPRRRSQRESQC 195

DB 162 RRGGRSPRRTPSPRRRSKSPRRRSQRESQC 195

DB 162 RRGGRSPRRTPSPRRRSKSPRRRSQRESQC 195

Matches 32; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRGRSPRRTPSPRRRSKSPRRRSQSRESOC 34  
DB 178 RRRGRSPRRTPSPRRRSKSPRRRSQSRESOC 211

## RESULT 8

CORA\_HPBVW  
ID CORA\_HPBVW STANDARD; PRT; 185 AA.  
AC P03149;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 01-OCT-1989 (Rel. 12, Last annotation update)  
DE CORE ANTIGEN.  
GN C.

OS Hepatitis B virus (subtype adw).  
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.

OX NCBI\_TaxID=106821;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=83168919; PubMed=6300776;

RA Oho Y., Onda H., Sasada K., Igarashi K., Sugino Y., Nishiohara K.;

RT "The complete nucleotide sequences of the cloned hepatitis B virus

DNA; subtype adr and adw.";

RL Nucleic Acids Res. 11:1747-1757(1983).

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CC EMBL; V00866; ; NOT\_ANNOTATED\_CDS.

DR PIR; C93460; NKVL6.

DR InterPro: IPR002006; Hepatitis\_core.

DR Pfam: PF00906; Hepatitis\_core; 1.

KW Core protein; Repeat.

FT REPEAT 164 171

FT REPEAT 172 179

SQ SEQUENCE 185 AA; 21394 MW; B86A90D541BA70F9 CRC64;

Query Match 93.8%; Score 165; DB 1; Length 185;  
Best Local Similarity 94.1%; Pred. No. 1.1e-11;  
Matches 32; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RRRGRSPRRTPSPRRRSKSPRRRSQSRESOC 34  
DB 152 RRRGRSPRRTPSPRRRSKSPRRRSQSRESOC 185

## RESULT 9

CORA\_HPBV9  
ID CORA\_HPBV9 STANDARD; PRT; 214 AA.  
AC P17099;  
DT 01-AUG-1990 (Rel. 15, Created)  
DT 01-AUG-1990 (Rel. 15, Last sequence update)  
DT 01-AUG-1992 (Rel. 23, Last annotation update)  
DE CORE ANTIGEN.  
GN C.

OS Hepatitis B virus (subtype adw / strain 991).  
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.

OX NCBI\_TaxID=10410;

RN [1]

RP SEQUENCE FROM N.A.

RA Koehel H.G., Schueler A., Lottmann S., Thomsen R.;

RL Submitted (FEB-1990) to the EMBL/Genbank/DBJ databases.

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CC EMBL; X51970; CAA36232.1; .

DR PIR; S10381; NKVLKS

DR InterPro: IPR002006; Hepatitis\_core.

DR Pfam: PF00906; Hepatitis\_core; 1.

KW Core protein; Repeat.

FT REPEAT 193 200

FT REPEAT 201 208

SQ SEQUENCE 214 AA; 24722 MW; 2D668333EC5AFB8C CRC64;

Query Match 93.8%; Score 165; DB 1; Length 214;  
Best Local Similarity 94.1%; Pred. No. 1.3e-11;  
Matches 32; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RRRGRSPRRTPSPRRRSKSPRRRSQSRESOC 34  
DB 181 RRRGRSPRRTPSPRRRSKSPRRRSQSRESOC 214

## RESULT 10

CORA\_HPBVL

ID CORA\_HPBVL STANDARD; PRT; 183 AA.

AC P12901;

DT 01-OCT-1989 (Rel. 12, Created)

DT 01-OCT-1989 (Rel. 12, Last sequence update)

DT 01-APR-1990 (Rel. 14, Last annotation update)

DE CORE ANTIGEN.

GN C.

OS Hepatitis B virus (strain lsh / chimpanzee isolate).

OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.

OX NCBI\_TaxID=10414;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=88258473; PubMed=2838576;

RA Vaadin M., Wolstenholme A.J., Tsiuquaye K.N., Zuckerman A.J.;

RA Harrison T.J.;

RT "The complete nucleotide sequence of the genome of a hepatitis B

virus isolated from a naturally infected chimpanzee.";

RL J. Gen. Virol. 69:1383-1389(1988).

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CC EMBL; D00220; BAA00157.1; .

DR PIR; A28885; NKVLCP

DR InterPro: IPR002006; Hepatitis\_core.

DR Pfam: PF00906; Hepatitis\_core; 1.

KW Core protein; Repeat.

FT REPEAT 162 169

FT REPEAT 170 177

SQ SEQUENCE 183 AA; 20999 MW; 923DCB94A33FC0E8 CRC64;

Query Match 90.3%; Score 159; DB 1; Length 183;  
Best Local Similarity 91.2%; Pred. No. 4.8e-11;  
Matches 31; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 RRRGRSPRRTPSPRRRSKSPRRRSQSRESOC 34  
DB 150 RRRGRSPRRTPSPRRRSKSPRRRSQSRESOC 183

```

RESULT 11
CORAHBPV2
ID CORAHBPV2 STANDARD; PRT; 212 AA.
AC Q05495;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE CORE ANTIGEN.
GN Hepatitis B virus (subtype adw4 / strain Brazil / isolate w4B).
OS Viruses; Retroviral viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=45410;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93346970; PubMed=8345355;
RA Naumann H., Schaefer S., Yoshida C.F.T., Gaspar A.M.C., Repp R.,
RA Gerlich W.H.;
RT "Identification of a new hepatitis B virus (HBV) genotype from Brazil
RT that expresses HBV surface antigen subtype adw4.";
RL J. Gen. Virol. 74:1637-1632(1993).
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CC -----
DR EMBL; X69798; CAA49452.1;
DR InterPro: IPR002006; Hepatitis_core.
DR Pfam: PF00906; Hepatitis_core; 1.
KW Core protein; Repeat.
FT DOMAIN 178 204 ARG-RICH.
FT DOMAIN 184 203 3 X 5 AA REPEATS OF S-P-R-R-R.
FT REPEAT 184 188 1.
FT REPEAT 184 188 1.
FT REPEAT 191 195 2.
FT REPEAT 199 203 3.
SQ SEQUENCE 212 AA; 24234 MW; F032610B7C36FD2 CRC64;

Query Match 90.3%; Score 159; DB 1; Length 212;
Best Local Similarity 91.2%; Pred. No. 5.5e-11;
Matches 31; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 RRRGRSPRRTPSPRRRSKSPRRRSQSRSQC 34
| | | | | | | | | | | | | | | | | | | | |
DB 179 RRRGRSPRRTPSPRRRSKSPRRRSQSRSQC 212
| | | | | | | | | | | | | | | | | | | | |

RESULT 12
CORAHBPV2
ID CORAHBPV2 STANDARD; PRT; 185 AA.
AC P03148;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE CORE ANTIGEN.
GN Hepatitis B virus (subtype adw2).
OS Viruses; Retroviral viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10408;
RN [1]
RP SEQUENCE FROM N.A.
RX Valenzuela P., Quiroga M., Zaldivar J., Gray P., Rutter W.J.;
RA (in) Field B.N., Jaenisch R., Fox C.F. (eds.);
RL Animal virus genetics, pp.57-70, Academic Press, New York (1980).
DR PIR; A94409; NKVL43.
DR InterPro: IPR002006; Hepatitis_core.
DR Pfam: PF00906; Hepatitis_core; 1.
KW Core protein; Repeat.
FT REPEAT 164 171
FT REPEAT 172 179

Query Match 80.4%; Score 141.5; DB 1; Length 217;
Best Local Similarity 76.9%; Pred. No. 4.3e-09;
Matches 30; Conservative 1; Mismatches 3; Indels 5; Gaps 1;

QY 1 RRRGRSPRRTPSPRRRSKSPRRRSQSRSQC 34
| | | | | | | | | | | | | | | | | | | | |
DB 179 RRRGRSRAARSRRTPSPRRRSKSPRRRSQSRSQC 217
| | | | | | | | | | | | | | | | | | | | |

RESULT 13
CORAHBPV2
ID CORAHBPV2 STANDARD; PRT; 217 AA.
AC P03153;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 01-JAN-1990 (Rel. 13, Last annotation update)
DE CORE ANTIGEN.
GN Ground squirrel hepatitis virus (GSHV).
OS Viruses; Retroviral viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10406;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=84267998; PubMed=6086950;
RA Seeger C., Ganem D., Varmus H.E.;
RT "Nucleotide sequence of an infectious molecularly cloned genome of
RT ground squirrel hepatitis virus.";
RL J. Virol. 51:367-375(1984).
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CC -----
DR EMBL; K02715; AAA46755.1;
DR PIR; A03715; NKVL5.
DR InterPro: IPR002006; Hepatitis_core.
DR Pfam: PF00906; Hepatitis_core; 1.
KW Core protein; Repeat.
FT REPEAT 196 203
FT REPEAT 204 211
SQ SEQUENCE 217 AA; 25189 MW; DF489467355EC11A CRC64;

Query Match 89.8%; Score 158; DB 1; Length 185;
Best Local Similarity 91.2%; Pred. No. 6.2e-11;
Matches 31; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 RRRGRSPRRTPSPRRRSKSPRRRSQSRSQC 34
| | | | | | | | | | | | | | | | | | | | |
DB 152 RRRGRSPRRTPSPRRRSKSPRRRSQSRSQC 185
| | | | | | | | | | | | | | | | | | | | |

RESULT 14
CORAHBPV1
ID CORAHBPV1 STANDARD; PRT; 188 AA.
AC P03152;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 13-DEC-1998 (Rel. 37, Last annotation update)
DE CORE ANTIGEN.
GN Woodchuck hepatitis virus 1 (WHV 1).
OS Woodchuck hepatitis virus 7 (WHV 7), and
OS Woodchuck hepatitis virus 59 (WHV 59), and
OS Woodchuck hepatitis virus 8 (infectious clone) (WHV 8).
OS Viruses; Retroviral viruses; Hepadnaviridae; Orthohepadnavirus.

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```

OX NCBI_TaxID-10430, 10432, 10431, 10434;
RN [1]
RP SEQUENCE FROM N.A.
RX SPECIES-Woodchuck hepatitis virus 1;
RA MEDLINE-82216969; PubMed-7086958;
RT Galibert F., Chen T.N., Mandart E.;
RT "Nucleotide sequence of a cloned woodchuck hepatitis virus genome:
RT comparison with the hepatitis B virus sequence.";
RL J. Virol. 41:51-65(1982).
RN [2]
RP SEQUENCE FROM N.A.
RX SPECIES-Woodchuck hepatitis virus 7, and Woodchuck hepatitis virus 59;
RA MEDLINE-88101359; PubMed-3336938;
RT Cohen J.I., Miller R.H., Rosenblum B., Denniston K., Gerin J.L.,
RT Purcell R.H.;
RT "Sequence comparison of woodchuck hepatitis virus replicative forms
RT shows conservation of the genome.";
RL Virology 162:12-20(1988).
RN [3]
RP SEQUENCE FROM N.A.
RX SPECIES-Woodchuck hepatitis virus 8 (infectious clone);
RA MEDLINE-89184524; PubMed-2928306;
RT Girones R., Cote P.J., Hornbuckle W.E., Tennant B.C., Gerin J.L.,
RT Purcell R.H., Miller R.H.;
RT "Complete nucleotide sequence of a molecular clone of woodchuck
RT hepatitis virus that is infectious in the natural host.";
RL Proc. Natl. Acad. Sci. U.S.A. 86:1846-1849(1989).
CC
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CC -----
DR EMBL; J02442; AAA46761.1; -
DR EMBL; M18752; AAA46769.1; -
DR EMBL; M19183; AAA46765.1; -
DR EMBL; J04514; AAA46772.1; -
DR PIR; A03713; NKVLC.
DR PIR; C32397; NKVLC.
DR PIR; C32397; NKVLC3.
DR InterPro; IPR002006; Hepatitis_core.
DR Pfam; PF00906; Hepatitis_core; 1.
KW Core Protein; Repeat.
FT REPEAT 167 174
FT REPEAT 175 182
SQ SEQUENCE 188 AA; 21693 MW; 1F4454D0A7B7CE42 CRC64;

Query Match 79.3%; Score 139.5; DB 1; Length 188;
Best Local Similarity 74.4%; Pred. No. 6.2e-09;
Matches 29; Conservative 2; Mismatches 3; Indels 5; Gaps 1;

QY 1 RRG-----RSPRRTPSPRRRSKSPRRRSQSRSQC 34
   ||||| ||||| ||||| ||||| ||||| ||||| :
DB 150 RRGGARASPRRTTPSPRRRSQSRSQSRSQPSANC 188

RESULT 15
CORAWHV8
ID CORAWHV8 STANDARD; PRT; 187 AA.
AC P06433;
DT 01-JAN-1988 (Rel. 06, Created)
DI 01-JAN-1988 (Rel. 06, Last sequence update)
DT 01-OCT-1989 (Rel. 12, Last annotation update)
DE CORE ANTIGEN.
GN C.
OS Woodchuck hepatitis virus 8 (WHV 8).
OC Viruses; Retroviridae; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID-10433;

```

```

RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-86062931; PubMed-3855246;
RA Kodama K., Ogasawara N., Yoshikawa H., Murakami S.;
RT "Nucleotide sequence of a cloned woodchuck hepatitis virus genome:
RT evolutionary relationship between hepadnaviruses.";
RL J. Virol. 56:978-986(1985).
CC
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CC -----
DR EMBL; M11082; AAA19185.1; -
DR PIR; A03714; NKVLC2.
DR InterPro; IPR002006; Hepatitis_core.
DR Pfam; PF00906; Hepatitis_core; 1.
KW Core Protein; Repeat.
FT REPEAT 166 173
FT REPEAT 174 181
SQ SEQUENCE 187 AA; 21579 MW; D4BC446FF7163165 CRC64;

Query Match 76.7%; Score 135; DB 1; Length 187;
Best Local Similarity 78.8%; Pred. No. 1.9e-08;
Matches 26; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 2 RRGSPRRTPSPRRRSKSPRRRSQSRSQC 34
   ||||| ||||| ||||| ||||| ||||| ||||| :
DB 155 RASRSPRRTPSPRRRSQSRSQSRSQPSANC 187

Search completed: April 18, 2002, 09:28:49
Job time: 117 sec

```

Thu Apr 18 10:44:57 2002

us-08-841-657a-2.rsp

Page 7

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: April 18, 2002, 09:26:52 ; Search time 13.49 Seconds

(without alignments)  
191.989 Million cell updates/sec

Title: US-08-841-657A-2

Perfect score: 176

Sequence: 1 RRGSRPRRTSPRRRSKSPRRRSQSRESQC 34

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: PIR\_68:\*\*

1: Pir1:\*\*

2: Pir2:\*\*

3: Pir3:\*\*

4: Pir4:\*\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	176	100.0	183	2 S53152	core antigen - hep
2	172	97.7	183	1 NKVLA2	core antigen - hep
3	172	97.7	183	2 S53232	core antigen - hep
4	172	97.7	183	2 S53247	core antigen - hep
5	172	97.7	183	2 S53267	core antigen - hep
6	172	97.7	183	2 S53149	core antigen - hep
7	172	97.7	183	2 S53194	core antigen - hep
8	172	97.7	183	2 S53181	core antigen - hep
9	172	97.7	183	2 S23318	core antigen - hep
10	172	97.7	212	1 NKVLAAH	e antigen precursor
11	172	97.7	212	1 NKVLBH	e antigen precursor
12	172	97.7	212	1 NKVLAA4	e antigen precursor
13	172	97.7	212	1 NKVLJ1	e antigen precursor
14	172	97.7	212	1 NKVLJ2	e antigen precursor
15	172	97.7	212	2 S53211	e antigen precursor
16	172	97.7	212	2 S53216	e antigen precursor
17	172	97.7	212	2 S53223	e antigen precursor
18	172	97.7	212	2 S53229	e antigen precursor
19	172	97.7	212	2 S53236	e antigen precursor
20	172	97.7	212	2 S53238	e antigen precursor
21	172	97.7	212	2 S53240	e antigen precursor
22	172	97.7	212	2 S53242	e antigen precursor
23	172	97.7	212	2 S53251	e antigen precursor
24	172	97.7	212	2 S53253	e antigen precursor
25	172	97.7	212	2 S53255	e antigen precursor
26	172	97.7	212	2 S53257	e antigen precursor
27	172	97.7	212	2 S53272	e antigen precursor
28	172	97.7	212	2 S53274	e antigen precursor
29	172	97.7	212	2 S53274	e antigen precursor

#### ALIGNMENTS

##### RESULT 1

S53152 core antigen - hepatitis B virus (isolate patient Tufariello'89)

N;Alternate names: HBC antigen

C;Species: core antigen

A;Variety: hepatitis B virus, HBV

C;Date: 08-Jul-1995 #sequence\_revision 03-Aug-1995 #text\_change 26-Aug-1999

C;Accession: S53152

R;Ref: M.E.; Mazzoleni, A.P.; Porru, A.; Balestrieri, A.

submitted to the EMBL Data Library, March 1995

A;Reference number: S53112

A;Accession: S53152

A;Molecule type: DNA

A;Residues: 1-183 <LAI>

A;Cross-references: EMBL:X85269; NID:g736033; PTDN:CAA59556.1; PID:g736036

A;Experimental source: Isolate patient Tufariello'89

A;Note: due to a stop codon between the alternative initiators the e antigen precursor

C;Genetics:

A;Gene: C

C;Superfamily: hepatitis B virus core antigen

C;Keywords: Core protein

Query Match 100.0%; Score 176; DB 2; Length 183;  
Best Local Similarity 100.0%; Pred. No. 4e-11;  
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRGSRPRRTSPRRRSKSPRRRSQSRESQC 34

Db 150 RRGSRPRRTSPRRRSKSPRRRSQSRESQC 183

##### RESULT 2

NKVLA2

core antigen - hepatitis B virus (subtype adyw)

C;Species: hepatitis B virus, HBV

A;Variety: subtype adyw

C;Date: 30-Jun-1992 #sequence\_revision 30-Jun-1992 #text\_change 16-Jul-1999

C;Accession: B93217; A03711

R;Ref: Patek, M.; Goto, T.; Gilbert, W.; Zink, B.; Schaller, H.; MacKay, P.; Leadbetter, G

Nature 282, 575-579, 1979

A;Title: Hepatitis B virus genes and their expression in E. coli.

A;Reference number: A93217; MUID:81012115

A;Accession: B93217

A;Molecule type: DNA

A;Residues: 1-183 <PAS>

A;Cross-references: GB:J02202; NID:g329637; PTDN:AAA45486.1; PID:g329638

A;Experimental source: subtype adyw

A;Note: due to a stop codon between the alternative initiators the e antigen precursor

C;Genetics:

A;Gene: C

C:Superfamily: hepatitis B virus core antigen  
C:Keywords: core protein  
F:1-183/Product: core antigen #status predicted <MAT>

Query Match 97.7%; Score 172; DB 1; Length 183;  
Best Local Similarity 97.1%; Pred. No. 1e-10;  
Matches 33; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRGSPRRRTSPRRRSKSPRRRSQSRESQC 34  
|||||  
DB 150 RRGSPRRRTSPRRRSKSPRRRSQSRESQC 183

## RESULT 3

S53232  
core antigen - hepatitis B virus (isolate patient Dettori-2'87)  
N:Alternate names: HBC antigen  
N:Contains: core antigen  
C:Species: hepatitis B virus, HBV  
A:Variety: isolate patient Dettori-2'87  
C:Date: 08-Jul-1995 #sequence\_revision 03-Aug-1995 #text\_change 26-Aug-1999  
C:Accession: S53232  
R:Lai, M.E.; Mazzoleni, A.P.; Porru, A.; Balestrieri, A.  
submitted to the EMBL Data Library, March 1995  
A:Reference number: S53112  
A:Gene: C  
A:Superfamily: hepatitis B virus core antigen  
C:Keywords: core protein

A:Molecule type: DNA  
A:Residues: 1-183 <LAI>  
A:Cross-references: EMBL:X85299; NID:g736146; PIDN:CAA59629.1; PID:g736149  
A:Experimental source: isolate patient Dettori-2'87  
A:Note: due to a stop codon between the alternative initiators the e antigen precursor

C:Superfamily: hepatitis B virus core antigen  
C:Keywords: core protein

Query Match 97.7%; Score 172; DB 2; Length 183;  
Best Local Similarity 97.1%; Pred. No. 1e-10;  
Matches 33; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRGSPRRRTSPRRRSKSPRRRSQSRESQC 34  
|||||  
DB 150 RRGSPRRRTSPRRRSKSPRRRSQSRESQC 183

## RESULT 4

S53247  
core antigen - hepatitis B virus (isolate patient Flore-2'91)  
N:Alternate names: HBC antigen  
N:Contains: core antigen  
C:Species: hepatitis B virus, HBV  
A:Variety: isolate patient Flore-2'91  
C:Date: 08-Jul-1995 #sequence\_revision 03-Aug-1995 #text\_change 26-Aug-1999  
C:Accession: S53247  
R:Lai, M.E.; Mazzoleni, A.P.; Porru, A.; Balestrieri, A.  
submitted to the EMBL Data Library, March 1995  
A:Reference number: S53112  
A:Gene: C  
A:Superfamily: hepatitis B virus core antigen  
C:Keywords: core protein

A:Molecule type: DNA  
A:Residues: 1-183 <LAI>  
A:Cross-references: EMBL:X85305; NID:g736168; PIDN:CAA59642.1; PID:g736171  
A:Experimental source: isolate patient Flore-2'91  
A:Note: due to a stop codon between the alternative initiators the e antigen precursor

C:Superfamily: hepatitis B virus core antigen  
C:Keywords: core protein

Query Match 97.7%; Score 172; DB 2; Length 183;  
Best Local Similarity 97.1%; Pred. No. 1e-10;

Matches 33; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1 RRGSPRRRTSPRRRSKSPRRRSQSRESQC 34  
|||||  
DB 150 RRGSPRRRTSPRRRSKSPRRRSQSRESQC 183

## RESULT 5

S53267  
core antigen - hepatitis B virus (isolate patient Lucianoc'92)  
N:Alternate names: HBC antigen  
N:Contains: core antigen  
C:Species: hepatitis B virus, HBV  
A:Variety: isolate patient Lucianoc'92  
C:Date: 08-Jul-1995 #sequence\_revision 03-Aug-1995 #text\_change 26-Aug-1999  
C:Accession: S53267  
R:Lai, M.E.; Mazzoleni, A.P.; Porru, A.; Balestrieri, A.  
submitted to the EMBL Data Library, March 1995  
A:Reference number: S53112  
A:Gene: C  
A:Superfamily: hepatitis B virus core antigen  
C:Keywords: core protein

A:Molecule type: DNA  
A:Residues: 1-183 <LAI>  
A:Cross-references: EMBL:X85260; NID:g736197; PIDN:CAA59530.1; PID:g736200  
A:Experimental source: isolate patient Lucianoc'92  
A:Note: due to a stop codon between the alternative initiators the e antigen precursor

C:Superfamily: hepatitis B virus core antigen  
C:Keywords: core protein

Query Match 97.7%; Score 172; DB 2; Length 183;  
Best Local Similarity 97.1%; Pred. No. 1e-10;  
Matches 33; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRGSPRRRTSPRRRSKSPRRRSQSRESQC 34  
|||||  
DB 150 RRGSPRRRTSPRRRSKSPRRRSQSRESQC 183

## RESULT 6

S53149  
core antigen - hepatitis B virus (isolate patient Sini'90)  
N:Alternate names: HBC antigen  
N:Contains: core antigen  
C:Species: hepatitis B virus, HBV  
A:Variety: isolate patient Sini'90  
C:Date: 08-Jul-1995 #sequence\_revision 03-Aug-1995 #text\_change 26-Aug-1999  
C:Accession: S53149  
R:Lai, M.E.; Mazzoleni, A.P.; Porru, A.; Balestrieri, A.  
submitted to the EMBL Data Library, March 1995  
A:Reference number: S53112  
A:Gene: C  
A:Superfamily: hepatitis B virus core antigen  
C:Keywords: core protein

A:Molecule type: DNA  
A:Residues: 1-183 <LAI>  
A:Cross-references: EMBL:X85268; NID:g736029; PIDN:CAA59553.1; PID:g736032  
A:Experimental source: isolate patient Sini'90  
A:Note: due to a stop codon between the alternative initiators the e antigen precursor

C:Superfamily: hepatitis B virus core antigen  
C:Keywords: core protein

Query Match 97.7%; Score 172; DB 2; Length 183;  
Best Local Similarity 97.1%; Pred. No. 1e-10;  
Matches 33; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRGSPRRRTSPRRRSKSPRRRSQSRESQC 34  
|||||  
DB 150 RRGSPRRRTSPRRRSKSPRRRSQSRESQC 183



RESULT 7  
S53194  
core antigen - hepatitis B virus (isolate patient Italcoc'92)  
N:Alternate names: HBC antigen  
N:Contains: core antigen  
C:Species: hepatitis B virus, HBV  
A:Variety: isolate patient Italcoc'92  
C:Date: 08-Jul-1995 #sequence\_revision 03-Aug-1995 #text\_change 26-Aug-1999  
C:Accession: S53194  
R:Lai, M.E.; Mazzoleni, A.P.; Porru, A.; Balestrieri, A.  
submitted to the EMBL Data Library, March 1995  
A:Reference number: S53112  
A:Accession: S53194  
A:Molecule type: DNA  
A:Residues: 1-183 <LA1>  
A:Cross-references: EMBL:X85257; NID:G736091; PIDN:CAA59522.1; PID:G736094  
A:Experimental source: isolate patient Italcoc'92  
A:Note: due to a stop codon between the alternative initiators the e antigen precursor  
C:Genetics:  
A:Gene: C  
C:Superfamily: hepatitis B virus core antigen  
C:Keywords: core protein

Query Match 97.7%; Score 172; DB 2; Length 183;  
Best Local Similarity 97.1%; Pred. No. 1e-10;  
Matches 33; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 RRGSRPRRTSPRRRSKSPRRRSQSRESQC 34  
|||||  
Db 150 RRGSRPRRTSPRRRSKSPRRRSQSRESQC 183

RESULT 8  
S53181  
core antigen - hepatitis B virus  
N:Alternate names: HBC antigen  
N:Contains: core antigen  
C:Species: hepatitis B virus, HBV  
C:Date: 08-Jul-1995 #sequence\_revision 03-Aug-1995 #text\_change 26-Aug-1999  
R:Lai, M.E.; Mazzoleni, A.P.; Porru, A.; Balestrieri, A.  
submitted to the EMBL Data Library, March 1995  
A:Reference number: S53112  
A:Accession: S53181  
A:Molecule type: DNA  
A:Residues: 1-183 <LA1>  
A:Cross-references: EMBL:X85279; NID:G736073; PIDN:CAA59583.1; PID:G736076  
A:Experimental source: isolate patient Bitti'89  
A:Note: due to a stop codon between the alternative initiators the e antigen precursor  
C:Genetics:  
A:Gene: C  
C:Superfamily: hepatitis B virus core antigen  
C:Keywords: core protein

Query Match 97.7%; Score 172; DB 2; Length 183;  
Best Local Similarity 97.1%; Pred. No. 1e-10;  
Matches 33; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 RRGSRPRRTSPRRRSKSPRRRSQSRESQC 34  
|||||  
Db 150 RRGSRPRRTSPRRRSKSPRRRSQSRESQC 183

RESULT 9  
S22318

core antigen - hepatitis B virus (subtype ayw, isolate Sardinia)  
N:Alternate names: HBC antigen  
C:Species: hepatitis B virus, HBV  
A:Variety: subtype ayw, isolate Sardinia  
C:Date: 19-Feb-1994 #sequence\_revision 01-Nov-1996 #text\_change 26-Aug-1999  
C:Accession: S22318  
R:Lai, M.E.; Melis, A.; Mazzoleni, A.P.; Farci, P.; Balestrieri, A.  
Nucleic Acids Res. 19: 5078, 1991  
A:Title: Sequence analysis of hepatitis B virus genome of a new mutant of ayw subtype  
A:Reference number: S22317; MUID:92020153  
A:Accession: S22318  
A:Status: nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-183 <LA1>  
A:Cross-references: EMBL:X59795; NID:G313780; PIDN:CAA42464.1; PID:G313782  
A:Experimental source: subtype ayw, isolate Sardinia  
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, May 1991  
C:Genetics:  
A:Gene: C  
C:Superfamily: hepatitis B virus core antigen  
C:Keywords: core protein

Query Match 97.7%; Score 172; DB 2; Length 183;  
Best Local Similarity 97.1%; Pred. No. 1e-10;  
Matches 33; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 RRGSRPRRTSPRRRSKSPRRRSQSRESQC 34  
|||||  
Db 150 RRGSRPRRTSPRRRSKSPRRRSQSRESQC 183

RESULT 10  
NKVLAH  
e antigen precursor / core antigen - hepatitis B virus (subtype ayw4, isolate hb321 a  
N:Alternate names: HBe antigen precursor / HBC antigen; Pre-C/C antigen  
N:Contains: core antigen; e antigen  
C:Species: hepatitis B virus, HBV  
A:Variety: subtype ayw4, isolate hb321; isolate patient Ferracuti'83; isolate patient  
cheri'83  
C:Date: 18-Dec-1981 #sequence\_revision 08-Nov-1996 #text\_change 16-Jul-1999  
C:Accession: S47405; S53191; S53209; S53234; S53264; S53262; S53277; A03711  
R:Plucieniczak, A.  
submitted to the EMBL Data Library, August 1994  
A:Description: Molecular cloning and sequencing of two complete genomes of polish iso  
A:Reference number: S47404  
A:Accession: S47405  
A:Molecule type: DNA  
A:Residues: 1-212 <PLD>  
A:Cross-references: EMBL:D35716; NID:G527435; PIDN:CAA84786.1; PID:G527437  
A:Experimental source: subtype ayw4, isolate hb321  
R:Lai, M.E.; Mazzoleni, A.P.; Porru, A.; Balestrieri, A.  
submitted to the EMBL Data Library, March 1995  
A:Reference number: S53112  
A:Accession: S53191  
A:Molecule type: DNA  
A:Residues: 1-212 <LA1>  
A:Cross-references: EMBL:X85283; NID:G736088; PIDN:CAA59593.1; PID:G736090  
A:Experimental source: isolate patient Ferracuti'83  
A:Accession: S53209  
A:Molecule type: DNA  
A:Residues: 1-212 <LA2>  
A:Cross-references: EMBL:X85290; NID:G736114; PIDN:CAA59609.1; PID:G736116  
A:Experimental source: isolate patient Castag'83  
A:Accession: S53234  
A:Molecule type: DNA  
A:Residues: 1-212 <LA3>  
A:Cross-references: EMBL:X85300; NID:G736150; PIDN:CAA59631.1; PID:G736152  
A:Experimental source: isolate patient Sanna'84  
A:Accession: S53264  
A:Molecule type: DNA  
A:Residues: 1-212 <LA4>  
A:Cross-references: EMBL:X85313; NID:G736194; PIDN:CAA59659.1; PID:G736196

A:Experimental source: isolate patient Licheri-1/85

A:Accession: S53249

A:Molecule type: DNA

A:Residues: 1-212 <LA>

A:Cross-references: EMBL:X85306; NID:g736172; PIDN:CAA59644.1; PID:g736174

A:Experimental source: isolate patient Flore-1/86

A:Accession: S53262

A:Molecule type: DNA

A:Residues: 1-212 <LA>

A:Cross-references: EMBL:X85312; NID:g736191; PIDN:CAA59657.1; PID:g736193

A:Experimental source: isolate patient Licheri/83

A:Accession: S53277

A:Molecule type: DNA

A:Residues: 30-212 <LA7>

A:Cross-references: EMBL:X85317; NID:g736211; PIDN:CAA59669.1; PID:g736214

A:Experimental source: patient Giordo-2/86

A:Note: due to a stop codon between the alternative initiators the e antigen precursor

R:Galibert, F.; Mandart, E.; Fitoussi, F.; Tiollais, P.; Charnay, P.

Nature 281, 646-650, 1979

A:Title: Nucleotide sequence of the hepatitis B virus genome (subtype ayw) in E. coli.

A:Reference number: A93214; MUID:81012091

A:Accession: A03711

A:Molecule type: DNA

A:Residues: 1-212 <GAL>

A:Cross-references: GJ:J02203; NID:g329640; PIDN:AAA45489.1; PID:g329642

A:Experimental source: subtype ayw

C:Genetics:

A:Gene: C

C:Superfamily: hepatitis B virus core antigen

C:Keywords: alternative initiators; core protein

F:1-29/Domain: signal sequence #status predicted <SIG>

F:30-212/Product: core antigen #status predicted <CAG>

F:30-178/Product: e antigen #status predicted <EAG>

F:179-212/Domain: carboxyl-terminal propeptide #link EAG #status predicted <ECP>

Query Match 97.7%; Score 172; DB 1; Length 212;

Best Local Similarity 97.1%; Pred. No. 1.1e-10;

Matches 33; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRGRSPRRTPSPRRRSKSPRRRSQSRQSQ 34

|||||

DB 179 RRRGRSPRRTPSPRRRSKSPRRRSQSRQSQ 212

RESULT 11

NKVLBH

e antigen precursor / core antigen - hepatitis B virus (subtype ayw, strain PHB320)

N:Alternate names: HBe antigen precursor / HBe antigen; pre-C/C antigen

C:Species: hepatitis B virus, HBV

A:Variety: subtype ayw, strain PHB320

A:Note: host Homo sapiens (man)

C>Date: 17-Mar-1987 #sequence\_revision 08-Nov-1996 #text\_change 28-Jul-2000

A:Accession: A03712

R:Bichko, V.; Pushko, P.; Dreilina, D.; Pumpen, P.; Gren, E.

FEBS Lett. 185, 208-212, 1985

A:Title: Subtype ayw variant of hepatitis B virus: DNA primary structure analysis.

A:Reference number: A05237; MUID:85204397

A:Accession: A03712

A:Molecule type: DNA

A:Residues: 1-212 <BIC>

A:Cross-references: GB:X02496; NID:g62280; PIDN:CAB41698.1; PID:g4704318

A:Experimental source: subtype ayw, strain PHB320

C:Genetics:

A:Gene: C

C:Superfamily: hepatitis B virus core antigen

C:Keywords: alternative initiators; core protein

F:1-29/Domain: signal sequence #status predicted <SIG>

F:30-212/Product: core antigen #status predicted <CAG>

F:30-178/Product: e antigen #status predicted <EAG>

F:179-212/Domain: carboxyl-terminal propeptide #link EAG #status predicted <ECP>

Query Match

Best Local Similarity 97.7%; Score 172; DB 1; Length 212;

Matches 33; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRGRSPRRTPSPRRRSKSPRRRSQSRQSQ 34

|||||

DB 179 RRRGRSPRRTPSPRRRSKSPRRRSQSRQSQ 212

RESULT 12

NKVLAA

e antigen precursor / core antigen - hepatitis B virus (subtype adr and others)

N:Alternate names: HBe antigen precursor / HBe antigen; pre-C/C antigen

C:Species: hepatitis B virus, HBV

A:Variety: subtypes adr; adr4; adr; 09D09HCC

C>Date: 30-Jun-1992 #sequence\_revision 08-Nov-1996 #text\_change 28-Jul-2000

C:Accession: A93480; C28925; B93460; S35530; T13467; A03711

R:Fujiyama, A.; Miyano, A.; Miyano, A.; Nozaki, C.; Toneyama, T.; Ontomo, N.; Matsubara, K.

Nucleic Acids Res. 11, 4601-4610, 1983

A:Title: Cloning and structural analyses of hepatitis B virus DNAs, subtype adr.

A:Reference number: A93480; MUID:83246570

A:Accession: A93480

A:Molecule type: DNA

A:Residues: 1-212 <FOJ>

A:Cross-references: GB:X01587; NID:g59404; PIDN:CAA25745.1; PID:g59407

A:Experimental source: subtype adr4

R:Okamoto, H.; Tsuda, F.; Sakugawa, H.; Sastrosoewignjo, R.I.; Imai, M.; Miyakawa, Y.

J. Gen. Virol. 69, 2575-2583, 1988

A:Title: Typing hepatitis B virus by homology in nucleotide sequence: comparison of s

A:Reference number: JS0253; MUID:89010694

A:Accession: C28925

A>Status: translation not shown

A:Molecule type: DNA

A:Residues: 1-212 <ORA>

A:Cross-references: EMBL:D00331; NID:g221499

A:Experimental source: subtype adr, strain Indonesia/pIDW420

R:Ono, Y.; Onda, H.; Sasada, R.; Igarashi, K.; Sugino, Y.; Nishioka, K.

Nucleic Acids Res. 11, 1747-1757, 1983

A:Title: The complete nucleotide sequences of the cloned hepatitis B virus DNA; subtype

A:Reference number: A93460; MUID:83168919

A:Accession: B93460

A:Molecule type: DNA

A:Residues: 30-212 <ONO>

A:Cross-references: GB:V00867

A:Experimental source: subtype adr

A:Note: due to a missing start codon for pre-C the e antigen precursor cannot be prod

R:Mukaide, M.; Kumazawa, T.; Hoshi, A.; Kawaguchi, R.; Hiki, K.

Nucleic Acids Res. 20, 6105, 1992

A:Title: The complete nucleotide sequence of hepatitis B virus, subtype adr (SRADR) a

A:Reference number: S35527; MUID:93096607

A:Accession: S35530

A>Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-212 <MUK>

A:Cross-references: EMBL:D12980; NID:g221500; PIDN:BAA02357.1; PID:g221504

A:Experimental source: subtype adr

A:Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1992

R:Takahashi, K.; Akahane, Y.; Hino, K.; Ohta, Y.; Mishi, S.

Arch. Virol. 143, 2313-2326, 1998

A:Title: Hepatitis B virus genomic sequence in the circulation of hepatocellular carc

A:Reference number: 217684; MUID:99129050

A:Accession: T13467

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-212 <TAK>

A:Cross-references: EMBL:AB014368; NID:g3551304; PIDN:BA432862.1; PID:g3551306

A:Experimental source: Japanese patient with hepatocellular carcinoma isolate 09D09HC

C:Genetics:

A:Gene: C

C:Superfamily: hepatitis B virus core antigen

C:Keywords: alternative initiators; core protein

F:1-29/Domain: signal sequence #status predicted <SIG>  
F:30-212/Product: core antigen #status predicted <CAG>  
F:30-178/Product: e antigen #status predicted <EAG>  
F:179-212/Domain: carboxyl-terminal propeptide #link EAG #status predicted <ECP>

Query Match 97.7%; Score 172; DB 1; Length 212;  
Best Local Similarity 97.1%; Pred. No. 1.1e-10;  
Matches 33; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRGSPRRTPSPRRRSKSPRRRSQSRESQC 34  
|||||  
Db 179 RRRGSPRRTPSPRRRSKSPRRRSQSRESQC 212

## RESULT 13

NKVLJ1 e antigen precursor / core antigen - hepatitis B virus (subtype adv, strain Japan/PJDM23)

N:Alternate names: HBe antigen precursor / HBe antigen; pre-C/C antigen  
N:Contains: core antigen; e antigen

C:Species: hepatitis B virus, HBV

A:Variety: subtype adv, strain Japan/PJDM233

C:Date: 31-Mar-1990 #sequence\_revision 08-Nov-1996 #text\_change 14-Nov-1997

C:Accession: A28925

R:Okamoto, H.; Tsuda, F.; Sakugawa, H.; Sastrosowignjo, R.I.; Imai, M.; Miyakawa, Y.; M

J. Gen. Virol. 69, 2575-2583, 1988

A:Title: Typing hepatitis B virus by homology in nucleotide sequence: comparison of sur

A:Reference number: J0253; MUID:89010694

A:Accession: A28925

A:Status: translation not shown

A:Molecule type: DNA

A:Residues: 1-212 <OKA>

A:Cross-references: EMBL:D00329; NID:g221498

A:Experimental source: subtype adv, strain Japan/PJDM233

C:Genetics:

A:Gene: C

C:Superfamily: hepatitis B virus core antigen

C:Keywords: alternative initiators; core protein

F:1-29/Domain: signal sequence #status predicted <SIG>

F:30-212/Product: core antigen #status predicted <CAG>

F:30-178/Product: e antigen #status predicted <EAG>

F:179-212/Domain: carboxyl-terminal propeptide #link EAG #status predicted <ECP>

Query Match 97.7%; Score 172; DB 1; Length 212;  
Best Local Similarity 97.1%; Pred. No. 1.1e-10;  
Matches 33; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRGSPRRTPSPRRRSKSPRRRSQSRESQC 34  
|||||  
Db 179 RRRGSPRRTPSPRRRSKSPRRRSQSRESQC 212

## RESULT 14

NKVLJ2 e antigen precursor / core antigen - hepatitis B virus (subtype adv, strain Okinawa/PODW

N:Alternate names: HBe antigen precursor / HBe antigen; pre-C/C antigen

N:Contains: core antigen; e antigen

C:Species: hepatitis B virus, HBV

A:Variety: subtype adv, strain Okinawa/PODW282

C:Date: 31-Mar-1990 #sequence\_revision 08-Nov-1996 #text\_change 14-Nov-1997

C:Accession: B28925

R:Okamoto, H.; Tsuda, F.; Sakugawa, H.; Sastrosowignjo, R.I.; Imai, M.; Miyakawa, Y.; M

J. Gen. Virol. 69, 2575-2583, 1988

A:Title: Typing hepatitis B virus by homology in nucleotide sequence: comparison of sur

A:Reference number: J0253; MUID:89010694

A:Accession: B28925

A:Status: translation not shown

A:Molecule type: DNA

A:Residues: 1-212 <OKA>

A:Cross-references: EMBL:D00330; NID:g221498

A:Experimental source: subtype adv, strain Okinawa/PODW282

C:Genetics:

A:Gene: C  
C:Superfamily: hepatitis B virus core antigen  
C:Keywords: alternative initiators; core protein  
F:1-29/Domain: signal sequence #status predicted <SIG>  
F:30-212/Product: core antigen #status predicted <CAG>  
F:30-178/Product: e antigen #status predicted <EAG>  
F:179-212/Domain: carboxyl-terminal propeptide #link EAG #status predicted <ECP>

Query Match 97.7%; Score 172; DB 1; Length 212;  
Best Local Similarity 97.1%; Pred. No. 1.1e-10;  
Matches 33; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRGSPRRTPSPRRRSKSPRRRSQSRESQC 34  
|||||  
Db 179 RRRGSPRRTPSPRRRSKSPRRRSQSRESQC 212

## RESULT 15

S53211

e antigen precursor / core antigen - hepatitis B virus (isolate patient Castag-1'85 a

N:Alternate names: HBe antigen; HBe antigen precursor / HBe antigen; pre-C/C antigen

N:Contains: core antigen; e antigen

C:Species: hepatitis B virus, HBV

A:Variety: isolate patient Castag-1'85; isolate patient Ferracuti-1'89

C:Date: 08-Jul-1995 #sequence\_revision 03-Aug-1995 #text\_change 26-Aug-1999

C:Accession: S53211; S53197

R:Lai, M.E.; Mazzoleni, A.P.; Porru, A.; Balestrieri, A.

submitted to the EMBL Data Library, March 1995

A:Reference number: S53112

A:Accession: S53211

A:Molecule type: DNA

A:Residues: 1-212 <LAI>

A:Cross-references: EMBL:X85291; NID:g736117; PIDN:CAA59611.1; PID:g736119

A:Experimental source: isolate patient Castag-1'85

A:Accession: S53197

A:Molecule type: DNA

A:Residues: 30-212 <LAW>

A:Cross-references: EMBL:X85284; NID:g736095; PIDN:CAA59596.1; PID:g736098

A:Experimental source: isolate patient Ferracuti-1'89

A:Note: due to a stop codon between the alternative initiators the e antigen precurs

C:Genetics:

A:Gene: C

C:Superfamily: hepatitis B virus core antigen

C:Keywords: alternative initiators; core protein

F:1-29/Domain: signal sequence #status predicted <SIG>

F:30-212/Product: core antigen #status predicted <CAG>

F:30-178/Product: e antigen #status predicted <EAG>

F:179-212/Domain: carboxyl-terminal propeptide #link EAG #status predicted <ECP>

Query Match 97.7%; Score 172; DB 2; Length 212;  
Best Local Similarity 97.1%; Pred. No. 1.1e-10;  
Matches 33; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRGSPRRTPSPRRRSKSPRRRSQSRESQC 34  
|||||  
Db 179 RRRGSPRRTPSPRRRSKSPRRRSQSRESQC 212

Search completed: April 18, 2002, 09:27:44  
Job time: 52 sec



GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 18, 2002, 09:26:52 ; Search time 22.03 Seconds  
(without alignments)  
225.749 Million cell updates/sec

Title: US-08-841-657A-2

Perfect score: 176

Sequence: 1 RRRGRSPRRTPSPRRRRKSPRRRRSQSRESQC 34

Scoring table: BLOSUM62

Gapop 10.0., Gapext 0.5

Searched: 473505 seqs, 146272329 residues

Total number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL\_17.\*

- 1: sp\_archaea.\*
- 2: sp\_bacteria.\*
- 3: sp\_fungi.\*
- 4: sp\_human.\*
- 5: sp\_invertebrate.\*
- 6: sp\_mammal.\*
- 7: sp\_mmc.\*
- 8: sp\_organelle.\*
- 9: sp\_phage.\*
- 10: sp\_plant.\*
- 11: sp\_rodent.\*
- 12: sp\_virus.\*
- 13: sp Vertebrate.\*
- 14: sp\_unclassified.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	176	100.0	96	12	Q9YL95
2	176	100.0	183	12	Q9YL92
3	176	100.0	183	12	Q9YL92
4	172	97.7	157	12	Q9WJC3
5	172	97.7	163	12	Q9WJC3
6	172	97.7	183	12	Q9WJC3
7	172	97.7	183	12	Q9WJC3
8	172	97.7	183	12	Q9WJC3
9	172	97.7	183	12	Q9WJC3
10	172	97.7	183	12	Q9WJC3
11	172	97.7	183	12	Q9WJC3
12	172	97.7	183	12	Q9WJC3
13	172	97.7	183	12	Q9WJC3
14	172	97.7	183	12	Q9WJC3
15	172	97.7	183	12	Q9WJC3
16	172	97.7	183	12	Q9WJC3
17	172	97.7	183	12	Q9WJC3
18	172	97.7	183	12	Q9WJC3
19	172	97.7	183	12	Q9WJC3

20	172	97.7	183	12	Q9YL95
21	172	97.7	183	12	Q9YL92
22	172	97.7	183	12	Q9YL92
23	172	97.7	183	12	Q9WJC3
24	172	97.7	183	12	Q9WJC3
25	172	97.7	183	12	Q9WJC3
26	172	97.7	183	12	Q9WJC3
27	172	97.7	183	12	Q9WJC3
28	172	97.7	183	12	Q9WJC3
29	172	97.7	183	12	Q9WJC3
30	172	97.7	183	12	Q9WJC3
31	172	97.7	183	12	Q9WJC3
32	172	97.7	183	12	Q9WJC3
33	172	97.7	183	12	Q9WJC3
34	172	97.7	183	12	Q9WJC3
35	172	97.7	183	12	Q9WJC3
36	172	97.7	183	12	Q9WJC3
37	172	97.7	183	12	Q9WJC3
38	172	97.7	183	12	Q9WJC3
39	172	97.7	183	12	Q9WJC3
40	172	97.7	183	12	Q9WJC3
41	172	97.7	183	12	Q9WJC3
42	172	97.7	183	12	Q9WJC3
43	172	97.7	183	12	Q9WJC3
44	172	97.7	183	12	Q9WJC3
45	172	97.7	183	12	Q9WJC3

ALIGNMENTS

RESULT 1					
Q9YJ3	Q9YJ3	PRELIMINARY;	PRT;	96	AA.
AC	Q9YJ3				
DT	01-MAY-1999 (Tremblrel. 10, Created)				
DT	01-MAY-1999 (Tremblrel. 10, Last sequence update)				
DT	01-JUN-2001 (Tremblrel. 17, Last annotation update)				
DE	CORE ANTIGEN (FRAGMENT).				
GN	C.				
OS	Hepatitis B virus.				
OC	Viruses; Retroviral viruses; Hepadnaviridae; Orthohepadnavirus.				
OX	NCBI_TaxID=10407;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=GENOTYPE D;				
RA	Manzin A.				
RT	"An outbreak of fulminant hepatitis B in a haematologic unit (Pesaro, Italy), part 2."				
RL	Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.				
DR	EMBL: AJ010007; CAA08962.1; -				
DR	EMBL: AJ009994; CAA08936.1; -				
DR	EMBL: AJ009995; CAA08938.1; -				
DR	EMBL: AJ009996; CAA08940.1; -				
DR	EMBL: AJ009997; CAA08942.1; -				
DR	EMBL: AJ009998; CAA08944.1; -				
DR	EMBL: AJ009999; CAA08946.1; -				
DR	EMBL: AJ010000; CAA08948.1; -				
DR	EMBL: AJ010002; CAA08952.1; -				
DR	EMBL: AJ010003; CAA08954.1; -				
DR	EMBL: AJ010004; CAA08956.1; -				
DR	EMBL: AJ010005; CAA08958.1; -				
DR	EMBL: AJ010006; CAA08960.1; -				
DR	InterPro: IPR002006; Hepatitis_core.				
DR	Pfam: PF00906; Hepatitis_core; 1.				
FT	NON_TER				
SEQUENCE	96 AA; 11443 MW; FEA862E745196B9E CRC64;				

Query Match 100.0%; Score 176; DB 12; Length 96;  
Best Local Similarity 100.0%; Pred. No. 8.2e-15;  
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRGRSPRRRTSPRRRSKSPRRRSQSRESQC 34  
 Db 63 RRRGRSPRRRTSPRRRSKSPRRRSQSRESQC 96

RESULT 2  
 ID Q67973 PRELIMINARY; PRT; 183 AA.  
 AC Q67973;  
 DT 01-NOV-1996 (Tremblrel. 01, Created)  
 DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)  
 DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)  
 DE X. PREC AND C GENES (TUFARIELLO).  
 GN CORE.  
 OS Hepatitis B virus.  
 OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.  
 OX NCBI\_TaxID=10407;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-PATIENT TUFARIELLO'89;  
 RA Lai M.E., Mazzoleni A.P., Porru A., Balestrieri A.;  
 RL Submitted (MAR-1995) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: X55259; CAA59556.1; -  
 DR InterPro: IPR002006; Hepatitis\_core.  
 DR Pfam: PF00906; Hepatitis\_core; 1.  
 SQ SEQUENCE 183 AA; 21072 MW; 4E06CF2F39199A3 CRC64;

Query Match 100.0%; Score 176; DB 12; Length 183;  
 Best Local Similarity 100.0%; Pred. No. 1.4e-14;  
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRGRSPRRRTSPRRRSKSPRRRSQSRESQC 34  
 Db 150 RRRGRSPRRRTSPRRRSKSPRRRSQSRESQC 183

RESULT 3  
 ID Q81102 PRELIMINARY; PRT; 183 AA.  
 AC Q81102;  
 DT 01-NOV-1996 (Tremblrel. 01, Created)  
 DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)  
 DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)  
 DE CORE ANTIGEN.  
 OS Hepatitis B virus.  
 OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.  
 OX NCBI\_TaxID=10407;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC MEDLINE=83168919; PubMed=6300776;  
 RA Ono Y., Onda H., Sasada R., Igarashi K., Sugino Y., Nishioka K.;  
 RT "The complete nucleotide sequences of the cloned hepatitis B virus  
 DNA; subtype adr and adw";  
 RL Nucleic Acids Res. 11:1747-1757(1983).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC MEDLINE=85077616; PubMed=6510717;  
 RA Kobayashi M., Koike K.;  
 RT "Complete nucleotide sequence of hepatitis B virus DNA of subtype adr  
 and its conserved gene organization";  
 RL Gene 30:227-232(1984).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC MEDLINE=90356395; PubMed=2388835;  
 RA Takemura F., Ishii T., Fujii N., Uchida T.;  
 RT "Complete nucleotide sequence of hepatitis B virus";  
 RL Nucleic Acids Res. 18:4587-4587(1990).  
 DR EMBL: D00630; BAA00523.1; -  
 DR InterPro: IPR002006; Hepatitis\_core.  
 DR Pfam: PF00906; Hepatitis\_core; 1.  
 SQ SEQUENCE 183 AA; 21102 MW; B32B2BF3AF7ED4E8 CRC64;

Query Match 100.0%; Score 176; DB 12; Length 183;  
 Best Local Similarity 100.0%; Pred. No. 1.4e-14;  
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRGRSPRRRTSPRRRSKSPRRRSQSRESQC 34  
 Db 150 RRRGRSPRRRTSPRRRSKSPRRRSQSRESQC 183

RESULT 4  
 ID Q991J9 PRELIMINARY; PRT; 157 AA.  
 AC Q991J9;  
 DT 01-JUN-2001 (Tremblrel. 17, Created)  
 DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)  
 DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)  
 DE PRECORE/CORE PROTEIN.  
 OS Hepatitis B virus.  
 OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.  
 OX NCBI\_TaxID=10407;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC Dong J., Cheng J., Wang Q., Shi S., Zhang J., Xia X., Si C.;  
 RA "HBV quasiespecies: preC/C region as example";  
 RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF335747; AAK30091.1; -  
 SQ SEQUENCE 157 AA; 18109 MW; DE48B1F72AA52F8A CRC64;

Query Match 97.7%; Score 172; DB 12; Length 157;  
 Best Local Similarity 97.1%; Pred. No. 3.7e-14;  
 Matches 33; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRGRSPRRRTSPRRRSKSPRRRSQSRESQC 34  
 Db 124 RRRGRSPRRRTSPRRRSKSPRRRSQSRESQC 157

RESULT 5  
 ID Q91HC8 PRELIMINARY; PRT; 163 AA.  
 AC Q91HC8;  
 DT 01-OCT-2000 (Tremblrel. 15, Created)  
 DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)  
 DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)  
 DE PRE-CORE/CORE PROTEIN.  
 OS Hepatitis B virus (subtype adw2).  
 OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.  
 OX NCBI\_TaxID=10408;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=ADW2;  
 RA Cheng T., Chen M., Zhang J., Xia N.S.;  
 RT "HBV genome sequence from patient's serum of Xiamen, Fujian, China";  
 RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF233236; AAF82722.1; -  
 DR InterPro: IPR002006; Hepatitis\_core.  
 DR Pfam: PF00906; Hepatitis\_core; 2.  
 SQ SEQUENCE 163 AA; 18565 MW; 5D2E668C43076FFE CRC64;

Query Match 97.7%; Score 172; DB 12; Length 163;  
 Best Local Similarity 97.1%; Pred. No. 3.8e-14;  
 Matches 33; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRGRSPRRRTSPRRRSKSPRRRSQSRESQC 34  
 Db 130 RRRGRSPRRRTSPRRRSKSPRRRSQSRESQC 163

RESULT 6  
 Q89437

ID Q89437 PRELIMINARY; PRT; 183 AA.  
 AC Q89437;  
 DT 01-NOV-1996 (TREMELrel. 01, Created)  
 DT 01-NOV-1996 (TREMELrel. 01, Last sequence update)  
 DT 01-JUN-2001 (TREMELrel. 17, Last annotation update)  
 DE X, PREC AND C GENES (CASTAA 2).  
 GN CORE.  
 OS Hepatitis B virus (subtype ayw).  
 OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.  
 OX NCBI\_TaxID=10418;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-PATIENT CASTAA-2'87;  
 RA Lai M.E., Mazzoleni A.P., Porru A., Balestrieri A.;  
 RL Submitted (MAR-1995) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-AYW;  
 RA Karayiannis P.;  
 RL Submitted (DEC-1995) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-AYW;  
 RA Karayiannis P.;  
 RL Submitted (SEP-1995) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; X85289; CAA59607.1; -;  
 DR EMBL; X80925; CAA56888.1; -;  
 DR InterPro: IPR002006; Hepatitis\_core.  
 DR Pfam: PF00906; Hepatitis\_core; 1.  
 SQ SEQUENCE 183 AA; 21102 MW; 2BB902063F53228 CRC64;

Query Match 97.7%; Score 172; DB 12; Length 183;  
 Best Local Similarity 97.1%; Pred. No. 4.2e-14;  
 Matches 33; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 RRGSRPRRTSPRRRSQSPRRRSQSQ 34  
 Db 150 RRGSRPRRTSPRRRSQSPRRRSQSQ 183

RESULT 7  
 Q67970 PRELIMINARY; PRT; 183 AA.  
 ID Q67970;  
 DT 01-NOV-1996 (TREMELrel. 01, Created)  
 DT 01-NOV-1996 (TREMELrel. 01, Last sequence update)  
 DT 01-JUN-2001 (TREMELrel. 17, Last annotation update)  
 DE X, PREC AND C GENES (SINI).  
 GN CORE.  
 OS Hepatitis B virus.  
 OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.  
 OX NCBI\_TaxID=10407;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-PATIENT SINI'90;  
 RA Lai M.E., Mazzoleni A.P., Porru A., Balestrieri A.;  
 RL Submitted (MAR-1995) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; X85268; CAA59553.1; -;  
 DR InterPro: IPR002006; Hepatitis\_core.  
 DR Pfam: PF00906; Hepatitis\_core; 1.  
 SQ SEQUENCE 183 AA; 21108 MW; A3C21BD403676FF5 CRC64;

Query Match 97.7%; Score 172; DB 12; Length 183;  
 Best Local Similarity 97.1%; Pred. No. 4.2e-14;  
 Matches 33; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 RRGSRPRRTSPRRRSQSPRRRSQSQ 34  
 Db 150 RRGSRPRRTSPRRRSQSPRRRSQSQ 183

RESULT 8  
 Q67997 PRELIMINARY; PRT; 183 AA.  
 ID Q67997;  
 DT 01-NOV-1996 (TREMELrel. 01, Created)  
 DT 01-NOV-1996 (TREMELrel. 01, Last sequence update)  
 DT 01-JUN-2001 (TREMELrel. 17, Last annotation update)  
 DE X, PREC AND C GENES (BITTI).  
 GN CORE.  
 OS Hepatitis B virus.  
 OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.  
 OX NCBI\_TaxID=10407;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-PATIENT BITTI'89;  
 RA Lai M.E., Mazzoleni A.P., Porru A., Balestrieri A.;  
 RL Submitted (MAR-1995) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; X85279; CAA59593.1; -;  
 DR InterPro: IPR002006; Hepatitis\_core.  
 DR Pfam: PF00906; Hepatitis\_core; 1.  
 SQ SEQUENCE 183 AA; 21158 MW; F74F9B9B2FF90D7C CRC64;

Query Match 97.7%; Score 172; DB 12; Length 183;  
 Best Local Similarity 97.1%; Pred. No. 4.2e-14;  
 Matches 33; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 RRGSRPRRTSPRRRSQSPRRRSQSQ 34  
 Db 150 RRGSRPRRTSPRRRSQSPRRRSQSQ 183

RESULT 9  
 Q68006 PRELIMINARY; PRT; 183 AA.  
 ID Q68006;  
 DT 01-NOV-1996 (TREMELrel. 01, Created)  
 DT 01-NOV-1996 (TREMELrel. 01, Last sequence update)  
 DT 01-JUN-2001 (TREMELrel. 17, Last annotation update)  
 DE X, PREC AND C GENES (ITALOC).  
 GN CORE.  
 OS Hepatitis B virus.  
 OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.  
 OX NCBI\_TaxID=10407;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-PATIENT ITALOC'92;  
 RA Lai M.E., Mazzoleni A.P., Porru A., Balestrieri A.;  
 RL Submitted (MAR-1995) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; X85257; CAA59522.1; -;  
 DR InterPro: IPR002006; Hepatitis\_core.  
 DR Pfam: PF00906; Hepatitis\_core; 1.  
 SQ SEQUENCE 183 AA; 20996 MW; E391589B6AD747AF CRC64;

Query Match 97.7%; Score 172; DB 12; Length 183;  
 Best Local Similarity 97.1%; Pred. No. 4.2e-14;  
 Matches 33; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 RRGSRPRRTSPRRRSQSPRRRSQSQ 34  
 Db 150 RRGSRPRRTSPRRRSQSPRRRSQSQ 183

RESULT 10  
 Q68008 PRELIMINARY; PRT; 183 AA.  
 ID Q68008;  
 DT 01-NOV-1996 (TREMELrel. 01, Created)  
 DT 01-NOV-1996 (TREMELrel. 01, Last sequence update)  
 DT 01-JUN-2001 (TREMELrel. 17, Last annotation update)  
 DE X, PREC AND C GENES (FERRACUTI 1).  
 GN CORE.

OS Hepatitis B virus.  
 OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.  
 OX NCBI\_TaxID=10407;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-PATIENT FERRACUTI-1'89;  
 RA Lai M.E., Mazzoleni A.P., Porru A., Balestrieri A.;  
 RL Submitted (MAR-1995) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; X85284; CAA59596.1; -  
 DR InterPro: IPR002006; Hepatitis\_core.  
 DR Pfam: PF00906; Hepatitis\_core; 1.  
 SQ SEQUENCE 183 AA; 21102 MW; 50D8D9763F25E958 CRC64;

Query Match 97.7%; Score 172; DB 12; Length 183;  
 Best Local Similarity 97.1%; Pred. No. 4.2e-14;  
 Matches 33; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRGRSPRRTPSPRRRSKSPRRRSQSRESQC 34  
 |||||  
 DB 150 RRRGRSPRRTPSPRRRSKSPRRRSQSRESQC 183

## RESULT 11

Q68037 PRELIMINARY; PRT; 183 AA.  
 AC Q68037;  
 DT 01-NOV-1996 (TREMELREL. 01, Created)  
 DT 01-NOV-1996 (TREMELREL. 01, Last sequence update)  
 DT 01-JUN-2001 (TREMELREL. 17, Last annotation update)  
 DE X, PREC AND C GENES (DETTORI 2).  
 GN CORE.  
 OS Hepatitis B virus.  
 OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.  
 OX NCBI\_TaxID=10407;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-PATIENT DETTORI-2'87;  
 RA Lai M.E., Mazzoleni A.P., Porru A., Balestrieri A.;  
 RL Submitted (MAR-1995) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; X85299; CAA59629.1; -  
 DR InterPro: IPR002006; Hepatitis\_core.  
 DR Pfam: PF00906; Hepatitis\_core; 1.  
 SQ SEQUENCE 183 AA; 21161 MW; CD85663FE5F8B933 CRC64;

Query Match 97.7%; Score 172; DB 12; Length 183;  
 Best Local Similarity 97.1%; Pred. No. 4.2e-14;  
 Matches 33; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRGRSPRRTPSPRRRSKSPRRRSQSRESQC 34  
 |||||  
 DB 150 RRRGRSPRRTPSPRRRSKSPRRRSQSRESQC 183

## RESULT 12

Q68048 PRELIMINARY; PRT; 183 AA.  
 AC Q68048;  
 DT 01-NOV-1996 (TREMELREL. 01, Created)  
 DT 01-NOV-1996 (TREMELREL. 01, Last sequence update)  
 DT 01-JUN-2001 (TREMELREL. 17, Last annotation update)  
 DE X, PREC AND C GENES (FLORE 2).  
 GN CORE.  
 OS Hepatitis B virus.  
 OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.  
 OX NCBI\_TaxID=10407;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-PATIENT FLORE-2'91;  
 RA Lai M.E., Mazzoleni A.P., Porru A., Balestrieri A.;  
 RL Submitted (MAR-1995) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; X85305; CAA59642.1; -

Query Match 97.7%; Score 172; DB 12; Length 183;  
 Best Local Similarity 97.1%; Pred. No. 4.2e-14;  
 Matches 33; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

DR InterPro: IPR002006; Hepatitis\_core.  
 DR Pfam: PF00906; Hepatitis\_core; 1.  
 SQ SEQUENCE 183 AA; 21132 MW; E66F00FABBE4258 CRC64;

Query Match 97.7%; Score 172; DB 12; Length 183;  
 Best Local Similarity 97.1%; Pred. No. 4.2e-14;  
 Matches 33; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRGRSPRRTPSPRRRSKSPRRRSQSRESQC 34  
 |||||  
 DB 150 RRRGRSPRRTPSPRRRSKSPRRRSQSRESQC 183

RESULT 13  
 Q68064 PRELIMINARY; PRT; 183 AA.  
 AC Q68064;  
 DT 01-NOV-1996 (TREMELREL. 01, Created)  
 DT 01-NOV-1996 (TREMELREL. 01, Last sequence update)  
 DT 01-JUN-2001 (TREMELREL. 17, Last annotation update)  
 DE X, PREC AND C GENES (LUCIANOC).  
 GN CORE.  
 OS Hepatitis B virus.  
 OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.  
 OX NCBI\_TaxID=10407;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-PATIENT LUCIANOC'92;  
 RA Lai M.E., Mazzoleni A.P., Porru A., Balestrieri A.;  
 RL Submitted (MAR-1995) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; X85260; CAA59530.1; -  
 DR InterPro: IPR002006; Hepatitis\_core.  
 DR Pfam: PF00906; Hepatitis\_core; 1.  
 SQ SEQUENCE 183 AA; 21022 MW; E679001806718CCE CRC64;

Query Match 97.7%; Score 172; DB 12; Length 183;  
 Best Local Similarity 97.1%; Pred. No. 4.2e-14;  
 Matches 33; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRGRSPRRTPSPRRRSKSPRRRSQSRESQC 34  
 |||||  
 DB 150 RRRGRSPRRTPSPRRRSKSPRRRSQSRESQC 183

RESULT 14  
 Q68083 PRELIMINARY; PRT; 183 AA.  
 AC Q68083;  
 DT 01-NOV-1996 (TREMELREL. 01, Created)  
 DT 01-NOV-1996 (TREMELREL. 01, Last sequence update)  
 DT 01-JUN-2001 (TREMELREL. 17, Last annotation update)  
 DE HEPATITIS B VIRUS X, PREC AND C GENES (AMOROSO).  
 GN CORE.  
 OS Hepatitis B virus.  
 OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.  
 OX NCBI\_TaxID=10407;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-PATIENT AMOROSO'89;  
 RA Lai M.E., Mazzoleni A.P., Porru A., Balestrieri A.;  
 RL Submitted (MAR-1995) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; X85263; CAA59538.1; -  
 DR InterPro: IPR002006; Hepatitis\_core.  
 DR Pfam: PF00906; Hepatitis\_core; 1.  
 SQ SEQUENCE 183 AA; 21208 MW; 885D861DADA412AA CRC64;

Query Match 97.7%; Score 172; DB 12; Length 183;  
 Best Local Similarity 97.1%; Pred. No. 4.2e-14;  
 Matches 33; Conservative 1; Mismatches 0; Indels 0; Gaps 0;



OY 1 RRGSRPRRTTSPRRRRSKSPRRRSQSRESQC 34  
 |||||  
 Db 150 RRGSRPRRTTSPRRRRSKSPRRRSQSRESQC 183

## RESULT 15

ID Q69597 PRELIMINARY; PRT; 183 AA.  
 AC Q69597;  
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)  
 DE CORE PROTEIN.  
 GN C.  
 OS Hepatitis B virus.  
 OC Viruses; Retroviridae; Hepadnaviridae; Orthohepadnavirus.  
 OX NCBI\_taxid=10407;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-GENOTYPE C;  
 RX MEDLINE=94120723; PubMed=8291231;  
 RA Nordier H., Courouce A.M., Magnius L.O.;  
 RT "Complete genomes, phylogenetic relatedness, and structural proteins  
 of six strains of the hepatitis B virus, four of which represent two  
 new genotypes".  
 RL Virology 198;489-503(1994).  
 DR EMBL; X75665; CAA53361.1; -;  
 DR InterPro; IPR002006; Hepatitis\_core.  
 DR Pfam; PF00906; Hepatitis\_core; 1.  
 SQ SEQUENCE 183 AA; 21081 MW; ED2DB34B0A6B466D CRC64;

Query Match 97.7%; Score 172; DB 12; Length 183;  
 Best Local Similarity 97.1%; Pred. No. 4.2e-14;  
 Matches 33; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 RRGSRPRRTTSPRRRRSKSPRRRSQSRESQC 34  
 |||||  
 Db 150 RRGSRPRRTTSPRRRRSKSPRRRSQSRESQC 183

Search completed: April 18, 2002, 09:28:32  
 Job time: 100 sec